



RECEIVED

OCT 25 2002

SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Dellapenna, Dean
Collakova, Eva
Coughlan, Sean J.
Helentjaris, Timothy G.

<120> PHYTYL/PRENYLTRANSFERASE NUCLEIC ACIDS,
POLYPEPTIDES AND USES THEREOF

<130> 1095R

<140> 09/560,761

<141> 2000-04-28

<150> 09/307,460

<151> 1999-05-07

<160> 32

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1616

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (108)...(1286)

<400> 1

gttccttcaa aatcatttct ttctcttctt tgattcccaa agatcacttc tttgtctttg 60
atcttttgatt ttttttctct ctggcgtgaa ggaagaagct ttatttct atg gag tct 116
Met Glu Ser
1

ctg ctc tct agt tct tct ctt gtt tcc gct gct ggt ggg ttt tgt tgg 164
Leu Leu Ser Ser Ser Ser Leu Val Ser Ala Ala Gly Gly Phe Cys Trp
5 10 15

aag aag cag aat cta aag ctc cac tct tta tca gaa atc cga gtt ctg 212
Lys Lys Gln Asn Leu Lys Leu His Ser Leu Ser Glu Ile Arg Val Leu
20 25 30 35

cgt tgt gat tcg agt aaa gtt gtc gca aaa ccg aag ttt agg aac aat 260
Arg Cys Asp Ser Ser Lys Val Val Ala Lys Pro Lys Phe Arg Asn Asn
40 45 50

ctt gtt agg cct gat ggt caa gga tct tca ttg ttg ttg tat cca aaa 308
Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu Tyr Pro Lys
55 60 65

cat aag tcg aga ttt cgg gtt aat gcc act gcg ggt cag cct gag gct 356
His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln Pro Glu Ala

70	75	80	
ttc gac tcg aat agc aaa cag aag tct ttt aga gac tcg tta gat gcg Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser Leu Asp Ala 85 90 95			404
ttt tac agg ttt tct agg cct cat aca gtt att ggc aca gtg ctt agc Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr Val Leu Ser 100 105 110 115			452
att tta tct gta tct ttc tta gca gca gag aag gtt tct gat ata tct Ile Leu Ser Val Ser Phe Leu Ala Ala Glu Lys Val Ser Asp Ile Ser 120 125 130			500
cct tta ctt ttc act ggc atc ttg gag gct gtt gtt gca gct ctc atg Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala Ala Leu Met 135 140 145			548
atg aac att tac ata gtt ggg cta aat cag ttg tct gat gtt gaa ata Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp Val Glu Ile 150 155 160			596
gat aag gtt aac aag ccc tat ctt cca ttg gca tca gga gaa tat tct Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly Glu Tyr Ser 165 170 175			644
gtt aac acc ggc att gca ata gta gct tcc ttc tcc atc atg agt ttc Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile Met Ser Phe 180 185 190 195			692
tgg ctt ggg tgg att gtt ggt tca tgg cca ttg ttc tgg gct ctt ttt Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp Ala Leu Phe 200 205 210			740
gtg agt ttc atg ctc ggt act gca tac tct atc aat ttg cca ctt tta Val Ser Phe Met Leu Gly Thr Ala Tyr Ser Ile Asn Leu Pro Leu Leu 215 220 225			788
cgg tgg aaa aga ttt gca ttg gtt gca gca atg tgt atc ctc gct gtc Arg Trp Lys Arg Phe Ala Leu Val Ala Ala Met Cys Ile Leu Ala Val 230 235 240			836
cga gct att att gtt caa atc gcc ttt tat cta cat att cag aca cat Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile Gln Thr His 245 250 255			884
gtg ttt gga aga cca atc ttg ttc act agg cct ctt att ttc gcc act Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile Phe Ala Thr 260 265 270 275			932
gcg ttt atg agc ttt ttc tct gtc gtt att gca ttg ttt aag gat ata Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe Lys Asp Ile 280 285 290			980
cct gat atc gaa ggg gat aag ata ttc gga atc cga tca ttc tct gta Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser Phe Ser Val 295 300 305			1028

act ctg ggt cag aaa cgg gtg ttt tgg aca tgt gtt aca cta ctt caa	1076
Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr Leu Leu Gln	
310 315 320	
atg gct tac gct gtt gca att cta gtt gga gcc aca tct cca ttc ata	1124
Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser Pro Phe Ile	
325 330 335	
tgg agc aaa gtc atc tcg gtt gtg ggt cat gtt ata ctc gca aca act	1172
Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu Ala Thr Thr	
340 345 350 355	
ttg tgg gct cga gct aag tcc gtt gat ctg agt agc aaa acc gaa ata	1220
Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys Thr Glu Ile	
360 365 370	
act tca tgt tat atg ttc ata tgg aag ctc ttt tat gca gag tac ttg	1268
Thr Ser Cys Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Leu	
375 380 385	
ctg tta cct ttt ttg aag tgactgacat tagaagagaa gaagatggag	1316
Leu Leu Pro Phe Leu Lys	
390	
ataaaagaat aagtcatcac tatgcttctg tttttattac aagttcatga aattaggtag	1376
tgaactagtg aattagagtt ttattctgaa acatggcaga ctgcaaaaat atgtcaaaga	1436
tatgaatttc tgttgggtaa agaagtctct gcttgggcaa aatcttaagg ttcggtgtgt	1496
tgatataatg ctaagcgaag aaatcgattc tatgtagaaa tttccgaaac tatgtgtaaa	1556
catgtcagaa catctccatt ctatatcttc ttctgcaaga aagctctgtt tttatcacct	1616

<210> 2

<211> 393

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Glu Ser Leu Leu Ser Ser Ser Ser Leu Val Ser Ala Ala Gly Gly	
1 5 10 15	
Phe Cys Trp Lys Lys Gln Asn Leu Lys Leu His Ser Leu Ser Glu Ile	
20 25 30	
Arg Val Leu Arg Cys Asp Ser Ser Lys Val Val Ala Lys Pro Lys Phe	
35 40 45	
Arg Asn Asn Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu	
50 55 60	
Tyr Pro Lys His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln	
65 70 75 80	
Pro Glu Ala Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser	
85 90 95	
Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr	
100 105 110	
Val Leu Ser Ile Leu Ser Val Ser Phe Leu Ala Ala Glu Lys Val Ser	
115 120 125	
Asp Ile Ser Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala	
130 135 140	
Ala Leu Met Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp	
145 150 155 160	
Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly	
165 170 175	

Glu Tyr Ser Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile
 180 185 190
 Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp
 195 200 205
 Ala Leu Phe Val Ser Phe Met Leu Gly Thr Ala Tyr Ser Ile Asn Leu
 210 215 220
 Pro Leu Leu Arg Trp Lys Arg Phe Ala Leu Val Ala Ala Met Cys Ile
 225 230 235 240
 Leu Ala Val Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile
 245 250 255
 Gln Thr His Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile
 260 265 270
 Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe
 275 280 285
 Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser
 290 295 300
 Phe Ser Val Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr
 305 310 315 320
 Leu Leu Gln Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser
 325 330 335
 Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu
 340 345 350
 Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys
 355 360 365
 Thr Glu Ile Thr Ser Cys Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala
 370 375 380
 Glu Tyr Leu Leu Leu Pro Phe Leu Lys
 385 390

<210> 3
 <211> 1540
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (21)...(1217)

<221> misc_feature
 <222> (1)...(1540)
 <223> n = A,T,C or G

<400> 3
 cgcgttcgcc cggccaaggg atg gac gcg ctt cgc cta cgg ccg tcc ctc ctc 53
 Met Asp Ala Leu Arg Leu Arg Pro Ser Leu Leu
 1 5 10

 ccc gtg cgg ccc ggc gcg gcc cgc ccg cga gat cat ttt cta cca cca 101
 Pro Val Arg Pro Gly Ala Ala Arg Pro Arg Asp His Phe Leu Pro Pro
 15 20 25

 tgt tgt tcc ata caa cga aat ggt gaa gga cga att tgc ttt tct agc 149
 Cys Cys Ser Ile Gln Arg Asn Gly Glu Gly Arg Ile Cys Phe Ser Ser
 30 35 40

 caa agg acc caa ggt cct acc ttg cat cac cat cag aaa ttc ttc gaa 197
 Gln Arg Thr Gln Gly Pro Thr Leu His His His Gln Lys Phe Phe Glu

45	50	55	
tgg aaa tcc tcc tat tgt agg ata tca cat cgg tca tta aat act tct			245
Trp Lys Ser Ser Tyr Cys Arg Ile Ser His Arg Ser Leu Asn Thr Ser			
60	65	70	75
ggt aat gct tcc ggg caa cag ctg cag tct gaa cct gaa aca cat gat			293
Val Asn Ala Ser Gly Gln Gln Leu Gln Ser Glu Pro Glu Thr His Asp			
	80	85	90
tct aca acc atc tgg agg gca ata tca tct tct cta gat gca ttt tac			341
Ser Thr Thr Ile Trp Arg Ala Ile Ser Ser Ser Leu Asp Ala Phe Tyr			
	95	100	105
aga ttt tcc cgg cca cat act gtc ata gga aca gca tta agc ata gtc			389
Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr Ala Leu Ser Ile Val			
	110	115	120
tca gtt tcc ctt cta gct gtc cag agc ttg tct gat ata tca cct ttg			437
Ser Val Ser Leu Leu Ala Val Gln Ser Leu Ser Asp Ile Ser Pro Leu			
	125	130	135
ttc ctc act ggt ttg ctg gag gca gtg gta gct gcc ctt ttc atg aat			485
Phe Leu Thr Gly Leu Leu Glu Ala Val Val Ala Ala Leu Phe Met Asn			
	140	145	150
atc tat att gtt gga ctg aac cag tta ttc gac att gag ata gac aag			533
Ile Tyr Ile Val Gly Leu Asn Gln Leu Phe Asp Ile Glu Ile Asp Lys			
	160	165	170
ggt aac aag cca act ctt cca ttg gca tct ggg gaa tac acc ctt gca			581
Val Asn Lys Pro Thr Leu Pro Leu Ala Ser Gly Glu Tyr Thr Leu Ala			
	175	180	185
act ggg gtt gca ata gtt tcc gtc ttt gcc gct atg agc ttt ggc ctt			629
Thr Gly Val Ala Ile Val Ser Val Phe Ala Ala Met Ser Phe Gly Leu			
	190	195	200
gga tgg gct gtt gga tca caa cct ctg ttt tgg gct ctt ttc ata agc			677
Gly Trp Ala Val Gly Ser Gln Pro Leu Phe Trp Ala Leu Phe Ile Ser			
	205	210	215
ttt gtt ctt ggg act gca tat tca atc aat ctg ccg tac ctt cga tgg			725
Phe Val Leu Gly Thr Ala Tyr Ser Ile Asn Leu Pro Tyr Leu Arg Trp			
	220	225	230
aag aga ttt gct gtt gtt gca gca ctg tgc ata tta gca gtt cgt gca			773
Lys Arg Phe Ala Val Val Ala Ala Leu Cys Ile Leu Ala Val Arg Ala			
	240	245	250
gtg att gtt cag ctg gcc ttt ttt ctc cac att cag act ttt gtt ttc			821
Val Ile Val Gln Leu Ala Phe Phe Leu His Ile Gln Thr Phe Val Phe			
	255	260	265
agg aga ccg gca gtg ttt tct agg cca tta tta ttt gca act gga ttt			869
Arg Arg Pro Ala Val Phe Ser Arg Pro Leu Leu Phe Ala Thr Gly Phe			
	270	275	280

atg acg ttc ttc tct gtt gta ata gca cta ttc aag gat ata cct gac	917
Met Thr Phe Phe Ser Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp	
285 290 295	
atc gaa ggg gac cgc ata ttc ggg atc cga tcc ttc agc gtc cgg tta	965
Ile Glu Gly Asp Arg Ile Phe Gly Ile Arg Ser Phe Ser Val Arg Leu	
300 305 310 315	
ggg caa aag aag gtc ttt tgg atc tgc gtt ggc ttg ctt gag atg gcc	1013
Gly Gln Lys Lys Val Phe Trp Ile Cys Val Gly Leu Leu Glu Met Ala	
320 325 330	
tac agc gtt gcg ata ctg atg gga gct acc tct tcc tgt ttg tgg agc	1061
Tyr Ser Val Ala Ile Leu Met Gly Ala Thr Ser Ser Cys Leu Trp Ser	
335 340 345	
aaa aca gca acc atc gct ggc cat tcc ata ctt gcc gcg atc cta tgg	1109
Lys Thr Ala Thr Ile Ala Gly His Ser Ile Leu Ala Ala Ile Leu Trp	
350 355 360	
agc tgc gcg cga tcg gtg gac ttg acg agc aaa gcc gca ata acg tcc	1157
Ser Cys Ala Arg Ser Val Asp Leu Thr Ser Lys Ala Ala Ile Thr Ser	
365 370 375	
ttc tac atg ttc atc tgg aag ctg ttc tac gcg gag tac ctg ctc atc	1205
Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile	
380 385 390 395	
cct ctg gtg cgg tgagcgcgag gcgaggtggt ggcagacgga tcggcgtcgg	1257
Pro Leu Val Arg	
cggggcgga aacaactcca cgggagaact tgagtgccgg aagtaaactc ccgtttgaaa	1317
gttgaagcgt gcaccaccgg caccgggcag agagagacac ggtggctgga tggatacgga	1377
tgccccccc aataaattcc cccgtgcatg gtacccccacg ctgcttgatg atatcccatg	1437
tgtccgggtg accggacctg atcgtctcta aanagattgg ttgcaaaaaa aaaaaaaaaa	1497
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aag	1540

<210> 4
 <211> 399
 <212> PRT
 <213> Zea mays

<400> 4
 Met Asp Ala Leu Arg Leu Arg Pro Ser Leu Leu Pro Val Arg Pro Gly
 1 5 10 15
 Ala Ala Arg Pro Arg Asp His Phe Leu Pro Pro Cys Cys Ser Ile Gln
 20 25 30
 Arg Asn Gly Glu Gly Arg Ile Cys Phe Ser Ser Gln Arg Thr Gln Gly
 35 40 45
 Pro Thr Leu His His His Gln Lys Phe Phe Glu Trp Lys Ser Ser Tyr
 50 55 60
 Cys Arg Ile Ser His Arg Ser Leu Asn Thr Ser Val Asn Ala Ser Gly
 65 70 75 80
 Gln Gln Leu Gln Ser Glu Pro Glu Thr His Asp Ser Thr Thr Ile Trp
 85 90 95
 Arg Ala Ile Ser Ser Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro
 100 105 110

His	Thr	Val	Ile	Gly	Thr	Ala	Leu	Ser	Ile	Val	Ser	Val	Ser	Leu	Leu
		115					120					125			
Ala	Val	Gln	Ser	Leu	Ser	Asp	Ile	Ser	Pro	Leu	Phe	Leu	Thr	Gly	Leu
		130				135					140				
Leu	Glu	Ala	Val	Val	Ala	Ala	Leu	Phe	Met	Asn	Ile	Tyr	Ile	Val	Gly
145					150					155					160
Leu	Asn	Gln	Leu	Phe	Asp	Ile	Glu	Ile	Asp	Lys	Val	Asn	Lys	Pro	Thr
				165					170					175	
Leu	Pro	Leu	Ala	Ser	Gly	Glu	Tyr	Thr	Leu	Ala	Thr	Gly	Val	Ala	Ile
			180					185					190		
Val	Ser	Val	Phe	Ala	Ala	Met	Ser	Phe	Gly	Leu	Gly	Trp	Ala	Val	Gly
		195				200						205			
Ser	Gln	Pro	Leu	Phe	Trp	Ala	Leu	Phe	Ile	Ser	Phe	Val	Leu	Gly	Thr
		210				215					220				
Ala	Tyr	Ser	Ile	Asn	Leu	Pro	Tyr	Leu	Arg	Trp	Lys	Arg	Phe	Ala	Val
225					230					235					240
Val	Ala	Ala	Leu	Cys	Ile	Leu	Ala	Val	Arg	Ala	Val	Ile	Val	Gln	Leu
				245					250					255	
Ala	Phe	Phe	Leu	His	Ile	Gln	Thr	Phe	Val	Phe	Arg	Arg	Pro	Ala	Val
			260					265					270		
Phe	Ser	Arg	Pro	Leu	Leu	Phe	Ala	Thr	Gly	Phe	Met	Thr	Phe	Phe	Ser
		275					280					285			
Val	Val	Ile	Ala	Leu	Phe	Lys	Asp	Ile	Pro	Asp	Ile	Glu	Gly	Asp	Arg
		290				295					300				
Ile	Phe	Gly	Ile	Arg	Ser	Phe	Ser	Val	Arg	Leu	Gly	Gln	Lys	Lys	Val
305					310					315					320
Phe	Trp	Ile	Cys	Val	Gly	Leu	Leu	Glu	Met	Ala	Tyr	Ser	Val	Ala	Ile
				325					330					335	
Leu	Met	Gly	Ala	Thr	Ser	Ser	Cys	Leu	Trp	Ser	Lys	Thr	Ala	Thr	Ile
			340					345					350		
Ala	Gly	His	Ser	Ile	Leu	Ala	Ala	Ile	Leu	Trp	Ser	Cys	Ala	Arg	Ser
		355					360					365			
Val	Asp	Leu	Thr	Ser	Lys	Ala	Ala	Ile	Thr	Ser	Phe	Tyr	Met	Phe	Ile
	370					375					380				
Trp	Lys	Leu	Phe	Tyr	Ala	Glu	Tyr	Leu	Leu	Ile	Pro	Leu	Val	Arg	
385					390					395					

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Arabidopsis thaliana

<400> 5
 ttgttttcag gctgtgttg cagctctc

28

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Arabidopsis thaliana

<400> 6

cgtttctgac ccagagttac agagaatg 28

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synechocystis

<400> 7
tattcatatg gcaactatcc aagctttttg 30

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synechocystis

<400> 8
ggatcctaat tgaagaagat actaaatagt tc 32

<210> 9
<211> 927
<212> DNA
<213> Synechocystis

<220>
<221> CDS
<222> (1)...(927)
<223>

<400> 9
atg gca act atc caa gct ttt tgg cgc ttc tcc cgc ccc cat acc atc 48
Met Ala Thr Ile Gln Ala Phe Trp Arg Phe Ser Arg Pro His Thr Ile
1 5 10 15

att ggt aca act ctg agc gtc tgg gct gtg tat ctg tta act att ctc 96
Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
20 25 30

ggg gat gga aac tca gtt aac tcc cct gct tcc ctg gat tta gtg ttc 144
Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
35 40 45

ggc gct tgg ctg gcc tgc ctg ttg ggt aat gtg tac att gtc ggc ctc 192
Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
50 55 60

aac caa ttg tgg gat gtg gac att gac cgc atc aat aag ccg aat ttg 240
Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
65 70 75 80

ccc cta gct aac gga gat ttt tct atc gcc cag ggc cgt tgg att gtg 288
Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
85 90 95

gga ctt tgt ggc gtt gct tcc ttg gcg atc gcc tgg gga tta ggg cta Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu 100 105 110	336
tgg ctg ggg cta acg gtg ggc att agt ttg att att ggc acg gcc tat Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr 115 120 125	384
tcg gtg ccg cca gtg agg tta aag cgc ttt tcc ctg ctg gcg gcc ctg Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu 130 135 140	432
tgt att ctg acg gtg cgg gga att gtg gtt aac ttg ggc tta ttt tta Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu 145 150 155 160	480
ttt ttt aga att ggt tta ggt tat ccc ccc act tta ata acc ccc atc Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile 165 170 175	528
tgg gtt ttg act tta ttt atc tta gtt ttc acc gtg gcg atc gcc att Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile 180 185 190	576
ttt aaa gat gtg cca gat atg gaa ggc gat cgg caa ttt aag att caa Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln 195 200 205	624
act tta act ttg caa atc ggc aaa caa aac gtt ttt cgg gga acc tta Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu 210 215 220	672
att tta ctc act ggt tgt tat tta gcc atg gca atc tgg ggc tta tgg Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp 225 230 235 240	720
gcg gct atg cct tta aat act gct ttc ttg att gtt tcc cat ttg tgc Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys 245 250 255	768
tta tta gcc tta ctc tgg tgg cgg agt cga gat gta cac tta gaa agc Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser 260 265 270	816
aaa acc gaa att gct agt ttt tat cag ttt att tgg aag cta ttt ttc Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe 275 280 285	864
tta gag tac ttg ctg tat ccc ttg gct ctg tgg tta cct aat ttt tct Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser 290 295 300	912
aat act att ttt tag Asn Thr Ile Phe * 305	927

<210> 10
 <211> 308
 <212> PRT
 <213> Synechocystis

<400> 10
 Met Ala Thr Ile Gln Ala Phe Trp Arg Phe Ser Arg Pro His Thr Ile
 1 5 10 15
 Ile Gly Thr Thr Leu Ser Val Trp Ala Val Tyr Leu Leu Thr Ile Leu
 20 25 30
 Gly Asp Gly Asn Ser Val Asn Ser Pro Ala Ser Leu Asp Leu Val Phe
 35 40 45
 Gly Ala Trp Leu Ala Cys Leu Leu Gly Asn Val Tyr Ile Val Gly Leu
 50 55 60
 Asn Gln Leu Trp Asp Val Asp Ile Asp Arg Ile Asn Lys Pro Asn Leu
 65 70 75 80
 Pro Leu Ala Asn Gly Asp Phe Ser Ile Ala Gln Gly Arg Trp Ile Val
 85 90 95
 Gly Leu Cys Gly Val Ala Ser Leu Ala Ile Ala Trp Gly Leu Gly Leu
 100 105 110
 Trp Leu Gly Leu Thr Val Gly Ile Ser Leu Ile Ile Gly Thr Ala Tyr
 115 120 125
 Ser Val Pro Pro Val Arg Leu Lys Arg Phe Ser Leu Leu Ala Ala Leu
 130 135 140
 Cys Ile Leu Thr Val Arg Gly Ile Val Val Asn Leu Gly Leu Phe Leu
 145 150 155 160
 Phe Phe Arg Ile Gly Leu Gly Tyr Pro Pro Thr Leu Ile Thr Pro Ile
 165 170 175
 Trp Val Leu Thr Leu Phe Ile Leu Val Phe Thr Val Ala Ile Ala Ile
 180 185 190
 Phe Lys Asp Val Pro Asp Met Glu Gly Asp Arg Gln Phe Lys Ile Gln
 195 200 205
 Thr Leu Thr Leu Gln Ile Gly Lys Gln Asn Val Phe Arg Gly Thr Leu
 210 215 220
 Ile Leu Leu Thr Gly Cys Tyr Leu Ala Met Ala Ile Trp Gly Leu Trp
 225 230 235 240
 Ala Ala Met Pro Leu Asn Thr Ala Phe Leu Ile Val Ser His Leu Cys
 245 250 255
 Leu Leu Ala Leu Leu Trp Trp Arg Ser Arg Asp Val His Leu Glu Ser
 260 265 270
 Lys Thr Glu Ile Ala Ser Phe Tyr Gln Phe Ile Trp Lys Leu Phe Phe
 275 280 285
 Leu Glu Tyr Leu Leu Tyr Pro Leu Ala Leu Trp Leu Pro Asn Phe Ser
 290 295 300
 Asn Thr Ile Phe
 305

<210> 11
 <211> 1278
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (106)...(879)

<400> 11

tcgcaaagac gctgcatgcc ttctatcagt tctgccgacc acacacaata tttggaacca	60
taataggcat tacttcggtg tctatcctgc cagtgaaga gcctg gac gat ttt acg	117
Asp Asp Phe Thr	
1	
ttg ata gct ata tgg gga ttt ctc gag gct ttg gcc gcc gca tta tgt	165
Leu Ile Ala Ile Trp Gly Phe Leu Glu Ala Leu Ala Ala Ala Leu Cys	
5 10 15 20	
atg aac gtt tat gta gta ggg ctg aac aag gtc aat aag cca acc ctc	213
Met Asn Val Tyr Val Val Gly Leu Asn Lys Val Asn Lys Pro Thr Leu	
25 30 35	
cca tta tcg ttc gga gag ttt tca atg cca act gca gta ttg tta gta	261
Pro Leu Ser Phe Gly Glu Phe Ser Met Pro Thr Ala Val Leu Leu Val	
40 45 50	
gtg gca ttc ttg gtc atg agc att agc atc gga ata aga tca aag tct	309
Val Ala Phe Leu Val Met Ser Ile Ser Ile Gly Ile Arg Ser Lys Ser	
55 60 65	
gct cca ttg atg tgt gct ttg ctt gtt tgc ttc ctt ctt gga agc gca	357
Ala Pro Leu Met Cys Ala Leu Leu Val Cys Phe Leu Leu Gly Ser Ala	
70 75 80	
tac ccc att gac gtc cca tta ctc cgg tgg aag cga cat gct ttt cta	405
Tyr Pro Ile Asp Val Pro Leu Leu Arg Trp Lys Arg His Ala Phe Leu	
85 90 95 100	
gct gca ttc tgc ata atc ttt gtg agg cct gta gtg gtc cag tta gct	453
Ala Ala Phe Cys Ile Ile Phe Val Arg Pro Val Val Val Gln Leu Ala	
105 110 115	
ttc ttt gca cac atg cag caa cat gtt ctg aag agg ccc ttg gca cct	501
Phe Phe Ala His Met Gln Gln His Val Leu Lys Arg Pro Leu Ala Pro	
120 125 130	
aca agg tcg gtg gtc ttt gca aca tgt ttc atg tgt tgc ttc gct gca	549
Thr Arg Ser Val Val Phe Ala Thr Cys Phe Met Cys Cys Phe Ala Ala	
135 140 145	
gta ata gcg cta ttc aag gat att cct gat gtc gat gga gat aga gat	597
Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Val Asp Gly Asp Arg Asp	
150 155 160	
ttc ggc att cag tcc atg act gta cga tta ggc caa cag aga gtg cat	645
Phe Gly Ile Gln Ser Met Thr Val Arg Leu Gly Gln Gln Arg Val His	
165 170 175 180	
agg ctc tgc att aat att ctc atg aca gca tac gca gcc gca att ttg	693
Arg Leu Cys Ile Asn Ile Leu Met Thr Ala Tyr Ala Ala Ala Ile Leu	
185 190 195	
gta ggc gcg tca tct acg aac ctg tat cag aag att gtc att gtg tct	741
Val Gly Ala Ser Ser Thr Asn Leu Tyr Gln Lys Ile Val Ile Val Ser	
200 205 210	
ggc cat ggc ttg ctt gcc tcc aca ctc tgg caa aga gca caa caa ttt	789

Gly	His	Gly	Leu	Leu	Ala	Ser	Thr	Leu	Trp	Gln	Arg	Ala	Gln	Gln	Phe		
		215					220					225					
gac att gag aat aag gat tgt atc aca caa ttt tat atg ttc att tgg																	837
Asp	Ile	Glu	Asn	Lys	Asp	Cys	Ile	Thr	Gln	Phe	Tyr	Met	Phe	Ile	Trp		
		230				235					240						
aag tta ttc tac gcc gag tat ttt ctt ata cca ttt gtg tag																	879
Lys	Leu	Phe	Tyr	Ala	Glu	Tyr	Phe	Leu	Ile	Pro	Phe	Val	*				
		245				250				255							
taaagaatca tgcgaagaac aacacccctg ctatagacat gtgaagggttt attgctaattg																	939
ttactctacc ccctgctata gacatgtgaa ggttttattgc taatgttact ctaccgaatg																	999
gtctgaatgt ctatgcgtca tttgaatgta atatgactat ttgttgtatc agggttaacaa																	1059
ctggagcaaaa tgtaccatgt atattaagca ttaattttaac tgcattcattt gtaccatgta																	1119
tattatgact atgtatgaga tattgtctct tattagtact ggatgtgatg tgtcttatta																	1179
tgactatgga tgagactttt gtgatgtaat tgatgagact atgggttttaa atattgttat																	1239
gtgattgtgt gtgagataaa aaaaaaaaaa aaaaaaaaaa																	1278
<210> 12																	
<211> 257																	
<212> PRT																	
<213> Zea mays																	
<400> 12																	
Asp	Asp	Phe	Thr	Leu	Ile	Ala	Ile	Trp	Gly	Phe	Leu	Glu	Ala	Leu	Ala		
1				5					10					15			
Ala	Ala	Leu	Cys	Met	Asn	Val	Tyr	Val	Val	Gly	Leu	Asn	Lys	Val	Asn		
			20					25					30				
Lys	Pro	Thr	Leu	Pro	Leu	Ser	Phe	Gly	Glu	Phe	Ser	Met	Pro	Thr	Ala		
		35				40						45					
Val	Leu	Leu	Val	Val	Ala	Phe	Leu	Val	Met	Ser	Ile	Ser	Ile	Gly	Ile		
	50				55						60						
Arg	Ser	Lys	Ser	Ala	Pro	Leu	Met	Cys	Ala	Leu	Leu	Val	Cys	Phe	Leu		
65					70					75					80		
Leu	Gly	Ser	Ala	Tyr	Pro	Ile	Asp	Val	Pro	Leu	Leu	Arg	Trp	Lys	Arg		
				85				90						95			
His	Ala	Phe	Leu	Ala	Ala	Phe	Cys	Ile	Ile	Phe	Val	Arg	Pro	Val	Val		
			100					105					110				
Val	Gln	Leu	Ala	Phe	Phe	Ala	His	Met	Gln	Gln	His	Val	Leu	Lys	Arg		
		115				120						125					
Pro	Leu	Ala	Pro	Thr	Arg	Ser	Val	Val	Phe	Ala	Thr	Cys	Phe	Met	Cys		
	130					135					140						
Cys	Phe	Ala	Ala	Val	Ile	Ala	Leu	Phe	Lys	Asp	Ile	Pro	Asp	Val	Asp		
145					150					155				160			
Gly	Asp	Arg	Asp	Phe	Gly	Ile	Gln	Ser	Met	Thr	Val	Arg	Leu	Gly	Gln		
			165					170						175			
Gln	Arg	Val	His	Arg	Leu	Cys	Ile	Asn	Ile	Leu	Met	Thr	Ala	Tyr	Ala		
		180						185					190				
Ala	Ala	Ile	Leu	Val	Gly	Ala	Ser	Ser	Thr	Asn	Leu	Tyr	Gln	Lys	Ile		
		195					200					205					
Val	Ile	Val	Ser	Gly	His	Gly	Leu	Leu	Ala	Ser	Thr	Leu	Trp	Gln	Arg		
	210					215					220						
Ala	Gln	Gln	Phe	Asp	Ile	Glu	Asn	Lys	Asp	Cys	Ile	Thr	Gln	Phe	Tyr		
225					230					235					240		
Met	Phe	Ile	Trp	Lys	Leu	Phe	Tyr	Ala	Glu	Tyr	Phe	Leu	Ile	Pro	Phe		
				245					250					255			
Val																	

<210> 13
 <211> 1771
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)...(1149)

<400> 13
 cca cgc gtc cgg gcc tcc ctt cct ctc ccg ccc agt act gcc gtc acc 48
 Pro Arg Val Arg Ala Ser Leu Pro Leu Pro Pro Ser Thr Ala Val Thr
 1 5 10 15
 gct cgc ttc ctc gcc gcc ccc gcc atc cgc gtg atc agc cca tcg agg 96
 Ala Arg Phe Leu Ala Ala Pro Ala Ile Arg Val Ile Ser Pro Ser Arg
 20 25 30
 ccc gcg ctg ccg ctc ctc tca tcc gcc tcc gca ggc ggc ttc cct cac 144
 Pro Ala Leu Pro Leu Leu Ser Ser Ala Ser Ala Gly Gly Phe Pro His
 35 40 45
 gcc tct cgc gct ccc tgc agt gcc gcc cgc gag cac cgc cgc ggc acc 192
 Ala Ser Arg Ala Pro Cys Ser Ala Ala Arg Glu His Arg Arg Gly Thr
 50 55 60
 gtg cgg gaa tgc tct cga gct gat gct gct gga gca gct cca tta tca 240
 Val Arg Glu Cys Ser Arg Ala Asp Ala Ala Gly Ala Ala Pro Leu Ser
 65 70 75 80
 aag aca ctg tta gac ctc aag gat tcc tgc tgg aga ttt tta agg cca 288
 Lys Thr Leu Leu Asp Leu Lys Asp Ser Cys Trp Arg Phe Leu Arg Pro
 85 90 95
 cat aca atc cga gga act gct tta gga tcc ata gca ttg gtt gcg aga 336
 His Thr Ile Arg Gly Thr Ala Leu Gly Ser Ile Ala Leu Val Ala Arg
 100 105 110
 gcc ttg ata gag aat tcc cat ctg ata aac tgg tgg ttg ata ttc aaa 384
 Ala Leu Ile Glu Asn Ser His Leu Ile Asn Trp Trp Leu Ile Phe Lys
 115 120 125
 gca ttc tat gga ctt ggg gca ttg ata ttt ggc aat ggt tac ata gtt 432
 Ala Phe Tyr Gly Leu Gly Ala Leu Ile Phe Gly Asn Gly Tyr Ile Val
 130 135 140
 ggg att aat cag atc tat gat gtt gct att gac aag gta aac aag cca 480
 Gly Ile Asn Gln Ile Tyr Asp Val Ala Ile Asp Lys Val Asn Lys Pro
 145 150 155 160
 tat tta ccc att gct gct ggt gat ctc tca att cag tca gca tgg ttg 528
 Tyr Leu Pro Ile Ala Ala Gly Asp Leu Ser Ile Gln Ser Ala Trp Leu
 165 170 175
 ttg gtg ata tta ttt gca gct gca ggt ttt tca att gtt ata tca aac 576

Leu Val Ile	Leu Phe Ala Ala Ala	Gly Phe Ser Ile Val Ile Ser Asn	
180		185 190	
ttt gga cct ttc att acc tct cta tac tgc ctt ggc cta ttt ctt ggc			624
Phe Gly Pro Phe Ile Thr Ser Leu Tyr Cys Leu Gly Leu Phe Leu Gly			
195	200	205	
act ata tat tct gtt cct cca ttt aga ctg aag aga tat ccg gtt gct			672
Thr Ile Tyr Ser Val Pro Pro Phe Arg Leu Lys Arg Tyr Pro Val Ala			
210	215	220	
gct ttt ctt atc att gca acg gtt cgt ggt ttc ctt ctc aac ttt ggc			720
Ala Phe Leu Ile Ile Ala Thr Val Arg Gly Phe Leu Leu Asn Phe Gly			
225	230	235	240
gtg tac tat gct act agg gct gca cta ggt ctt aca ttc caa tgg agc			768
Val Tyr Tyr Ala Thr Arg Ala Ala Leu Gly Leu Thr Phe Gln Trp Ser			
245	250	255	
tcc cct gtt gct ttc att aca tgc ttc gtg aca cta ttt gct ttg gtc			816
Ser Pro Val Ala Phe Ile Thr Cys Phe Val Thr Leu Phe Ala Leu Val			
260	265	270	
att gct ata acc aaa gat ctc cct gat gtt gaa gga gat cgc aag tat			864
Ile Ala Ile Thr Lys Asp Leu Pro Asp Val Glu Gly Asp Arg Lys Tyr			
275	280	285	
caa ata tca act ttg gca aca aag ctt ggt gtc aga aat att gca ttc			912
Gln Ile Ser Thr Leu Ala Thr Lys Leu Gly Val Arg Asn Ile Ala Phe			
290	295	300	
ctt gga tct ggt tta tta tta gca aac tat att gct gct att gct gta			960
Leu Gly Ser Gly Leu Leu Leu Ala Asn Tyr Ile Ala Ala Ile Ala Val			
305	310	315	320
gct ttt acc atg cct cag gat ttc agg tgc act gta atg gtt cct gtg			1008
Ala Phe Thr Met Pro Gln Asp Phe Arg Cys Thr Val Met Val Pro Val			
325	330	335	
cat gct gtc ctt gct ggt ggt tta att ttc cag aca tgg gtt ctg gag			1056
His Ala Val Leu Ala Gly Gly Leu Ile Phe Gln Thr Trp Val Leu Glu			
340	345	350	
caa gcg aag tac aga aag gat gct att tcg cag tac tat cgg ttc ata			1104
Gln Ala Lys Tyr Arg Lys Asp Ala Ile Ser Gln Tyr Tyr Arg Phe Ile			
355	360	365	
tgg aat ctc ttc tat gct gaa tat atc ttc ttc ccg tta ata tag			1149
Trp Asn Leu Phe Tyr Ala Glu Tyr Ile Phe Phe Pro Leu Ile *			
370	375	380	
agagatcttg tagttcatct tgatcttggg ctacagccta attcatggga gcaaatgaaa			1209
agaggagaaa gttggcaaaag tgaggtctgt tgtgcatatt ttcaacggaa acaatggagt			1269
agcaatattg ctatgctagg gttctgaagt tgtaggagct tttcgaagct tttacgatgt			1329
tgaaggcggtt gttgttggag ctgtggaagc tgtttttctt tttttccttt tgtatcaaca			1389
gtgtcgcggtt ctgtacggtc ttacttggaa gtgctttgac ctttgaacac atgggttgaa			1449
gcttgagatc tgggtccgaa cagatggcgg tggaacggcc aagacaagct tgtttcatgc			1509
cactcgaggt cgaggctaaa ccactacggc gtgctcttcc atgaaacgca gaaaactagg			1569

gaaatgacta tatatatggt gcaatacgtt gtatatatttc tgagtttcag ctcgtatata	1629
tagtaggaac ctcaactttt accccatcga ttggaagact gaaacttctt gcatgcgtat	1689
gtatgcctgt gggtatgtaa aaaccttggc ccgcacaaag ctacatgtta cagaactttc	1749
agctcaaaaa aaaaaaaaaa ag	1771

<210> 14
 <211> 382
 <212> PRT
 <213> Zea mays

<400> 14

Pro	Arg	Val	Arg	Ala	Ser	Leu	Pro	Leu	Pro	Pro	Ser	Thr	Ala	Val	Thr
1				5					10					15	
Ala	Arg	Phe	Leu	Ala	Ala	Pro	Ala	Ile	Arg	Val	Ile	Ser	Pro	Ser	Arg
		20						25					30		
Pro	Ala	Leu	Pro	Leu	Leu	Ser	Ser	Ala	Ser	Ala	Gly	Gly	Phe	Pro	His
		35					40					45			
Ala	Ser	Arg	Ala	Pro	Cys	Ser	Ala	Ala	Arg	Glu	His	Arg	Arg	Gly	Thr
	50					55					60				
Val	Arg	Glu	Cys	Ser	Arg	Ala	Asp	Ala	Ala	Gly	Ala	Ala	Pro	Leu	Ser
65					70					75				80	
Lys	Thr	Leu	Leu	Asp	Leu	Lys	Asp	Ser	Cys	Trp	Arg	Phe	Leu	Arg	Pro
				85					90					95	
His	Thr	Ile	Arg	Gly	Thr	Ala	Leu	Gly	Ser	Ile	Ala	Leu	Val	Ala	Arg
			100					105					110		
Ala	Leu	Ile	Glu	Asn	Ser	His	Leu	Ile	Asn	Trp	Trp	Leu	Ile	Phe	Lys
		115					120					125			
Ala	Phe	Tyr	Gly	Leu	Gly	Ala	Leu	Ile	Phe	Gly	Asn	Gly	Tyr	Ile	Val
	130					135				140					
Gly	Ile	Asn	Gln	Ile	Tyr	Asp	Val	Ala	Ile	Asp	Lys	Val	Asn	Lys	Pro
145				150						155				160	
Tyr	Leu	Pro	Ile	Ala	Ala	Gly	Asp	Leu	Ser	Ile	Gln	Ser	Ala	Trp	Leu
				165					170					175	
Leu	Val	Ile	Leu	Phe	Ala	Ala	Ala	Gly	Phe	Ser	Ile	Val	Ile	Ser	Asn
		180						185					190		
Phe	Gly	Pro	Phe	Ile	Thr	Ser	Leu	Tyr	Cys	Leu	Gly	Leu	Phe	Leu	Gly
		195					200					205			
Thr	Ile	Tyr	Ser	Val	Pro	Pro	Phe	Arg	Leu	Lys	Arg	Tyr	Pro	Val	Ala
	210					215					220				
Ala	Phe	Leu	Ile	Ile	Ala	Thr	Val	Arg	Gly	Phe	Leu	Leu	Asn	Phe	Gly
225					230					235				240	
Val	Tyr	Tyr	Ala	Thr	Arg	Ala	Ala	Leu	Gly	Leu	Thr	Phe	Gln	Trp	Ser
				245					250					255	
Ser	Pro	Val	Ala	Phe	Ile	Thr	Cys	Phe	Val	Thr	Leu	Phe	Ala	Leu	Val
			260					265					270		
Ile	Ala	Ile	Thr	Lys	Asp	Leu	Pro	Asp	Val	Glu	Gly	Asp	Arg	Lys	Tyr
		275					280					285			
Gln	Ile	Ser	Thr	Leu	Ala	Thr	Lys	Leu	Gly	Val	Arg	Asn	Ile	Ala	Phe
	290					295					300				
Leu	Gly	Ser	Gly	Leu	Leu	Ala	Asn	Tyr	Ile	Ala	Ala	Ile	Ala	Val	
305					310					315				320	
Ala	Phe	Thr	Met	Pro	Gln	Asp	Phe	Arg	Cys	Thr	Val	Met	Val	Pro	Val
				325					330					335	
His	Ala	Val	Leu	Ala	Gly	Gly	Leu	Ile	Phe	Gln	Thr	Trp	Val	Leu	Glu
			340					345					350		
Gln	Ala	Lys	Tyr	Arg	Lys	Asp	Ala	Ile	Ser	Gln	Tyr	Tyr	Arg	Phe	Ile
		355					360					365			
Trp	Asn	Leu	Phe	Tyr	Ala	Glu	Tyr	Ile	Phe	Phe	Pro	Leu	Ile		

370

375

380

<210> 15

<211> 1618

<212> DNA

<213> *Oryza sativa*

<220>

<221> CDS

<222> (59)...(1273)

<400> 15

gcacgagctt acaagccgcc gcgcgcgccc ggcgcgcgcg gtggtggcgg cggcggcg	58
atg gat tcg ctg cgc ctc cgg ccg tcg ctc ctc gcc gcg cgg gcc ccc	106
Met Asp Ser Leu Arg Leu Arg Pro Ser Leu Leu Ala Ala Arg Ala Pro	
1 5 10 15	
ggc gcg gcc tcg ctg ccg cct ctc cgg cga gat cac ttt cta cca cct	154
Gly Ala Ala Ser Leu Pro Pro Leu Arg Arg Asp His Phe Leu Pro Pro	
20 25 30	
tta tgt tct atc cat aga aat ggt aaa cgg cca gtt tct ttg tcc agc	202
Leu Cys Ser Ile His Arg Asn Gly Lys Arg Pro Val Ser Leu Ser Ser	
35 40 45	
caa agg acc caa ggt cct tcc ttc gat caa tgt cag aaa ttc ttt ggt	250
Gln Arg Thr Gln Gly Pro Ser Phe Asp Gln Cys Gln Lys Phe Phe Gly	
50 55 60	
tgg aaa tcc tcc cac cac agg ata cca cat cga cca aca tct agt tcc	298
Trp Lys Ser Ser His His Arg Ile Pro His Arg Pro Thr Ser Ser Ser	
65 70 75 80	
gct gac gct tcg gga caa cct cta caa tct tca gct gaa gca cat gat	346
Ala Asp Ala Ser Gly Gln Pro Leu Gln Ser Ser Ala Glu Ala His Asp	
85 90 95	
tca tca agt ata tgg aag cca ata tca tct tct ccg gat gca ttt tac	394
Ser Ser Ser Ile Trp Lys Pro Ile Ser Ser Ser Pro Asp Ala Phe Tyr	
100 105 110	
agg ttt tct cgg cca cat act gtc ata gga aca gca ctt agc ata gtc	442
Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr Ala Leu Ser Ile Val	
115 120 125	
tca gtt tcg ctg cta gct gtt gag aat ttg tcc gat gtg tct ccc ttg	490
Ser Val Ser Leu Leu Ala Val Glu Asn Leu Ser Asp Val Ser Pro Leu	
130 135 140	
ttc ctc act ggt ttg ctg gag gca gtg gta gca gct ctt ttc atg aac	538
Phe Leu Thr Gly Leu Leu Glu Ala Val Val Ala Ala Leu Phe Met Asn	
145 150 155 160	
atc tat atc gtt gga ttg aat cag ttg ttc gac att gag ata gat aag	586
Ile Tyr Ile Val Gly Leu Asn Gln Leu Phe Asp Ile Glu Ile Asp Lys	
165 170 175	

gtt aac aag cca act ctt cca tta gca tct ggg gaa tat tct cct gca	634
Val Asn Lys Pro Thr Leu Pro Leu Ala Ser Gly Glu Tyr Ser Pro Ala	
180 185 190	
act gga gtt gca ctt gta tca gcc ttc gct gct atg agc ttt ggc ctt	682
Thr Gly Val Ala Leu Val Ser Ala Phe Ala Ala Met Ser Phe Gly Leu	
195 200 205	
gga tgg gct gtt gga tca cag cct ctg ttc ctg gct ctt ttc att agc	730
Gly Trp Ala Val Gly Ser Gln Pro Leu Phe Leu Ala Leu Phe Ile Ser	
210 215 220	
ttt att ctt gga aca gca tat tcg att aat ctg cca ttc ctg aga tgg	778
Phe Ile Leu Gly Thr Ala Tyr Ser Ile Asn Leu Pro Phe Leu Arg Trp	
225 230 235 240	
aag aga tct gct gtt gtt gca gca ctt tgc ata tta gca gtc cgt gca	826
Lys Arg Ser Ala Val Val Ala Ala Leu Cys Ile Leu Ala Val Arg Ala	
245 250 255	
gtg att gtt cag ctg gca ttt ttt ctc cac att cag aca ttc gta ttc	874
Val Ile Val Gln Leu Ala Phe Phe Leu His Ile Gln Thr Phe Val Phe	
260 265 270	
aga aga cca gca gtc ttt acc agg cca ttg att ttt gca act gca ttc	922
Arg Arg Pro Ala Val Phe Thr Arg Pro Leu Ile Phe Ala Thr Ala Phe	
275 280 285	
atg acc ttt ttc tcc gtt gta ata gca ttg ttc aag gat ata cct gat	970
Met Thr Phe Phe Ser Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp	
290 295 300	
att gaa gga gac cgt att ttt ggt atc aaa tct ttc agt gtt cga tta	1018
Ile Glu Gly Asp Arg Ile Phe Gly Ile Lys Ser Phe Ser Val Arg Leu	
305 310 315 320	
ggg caa aag aag gtt ttc tgg att tgt gtt ggt ctg ctc gag atg gct	1066
Gly Gln Lys Lys Val Phe Trp Ile Cys Val Gly Leu Leu Glu Met Ala	
325 330 335	
tat tgt gtt gca ata ttg atg gga gct act tct gcc tgt ttg tgg agc	1114
Tyr Cys Val Ala Ile Leu Met Gly Ala Thr Ser Ala Cys Leu Trp Ser	
340 345 350	
aaa tac gca act gtg gtg gga cat gca atc ctt gcg gca atc cta tgg	1162
Lys Tyr Ala Thr Val Val Gly His Ala Ile Leu Ala Ala Ile Leu Trp	
355 360 365	
aac cgc tca cgg tcg att gat ctg aca agc aaa act gca atc act tct	1210
Asn Arg Ser Arg Ser Ile Asp Leu Thr Ser Lys Thr Ala Ile Thr Ser	
370 375 380	
ttc tac atg ttt atc tgg aag ctg ttc tac gcg gaa tac ctt ctc att	1258
Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile	
385 390 395 400	
cct ctt gta agg tga caaaggcgat tactccaggt agattggaat tggatcatgg	1313
Pro Leu Val Arg *	

ctggatggat	gaacggacgg	cgccccataa	aatcacctgc	aaatcacccg	gtacacatgt	1373
tgacatcctg	catccagata	tgatattgat	agatcatcgt	cggcaccatc	attcctctga	1433
aagatttcgc	acggcatttc	aacctccaac	tcccaacgta	ccccaaaaaa	agtaactagg	1493
ccaggtgagc	atctgctagc	ctatagtaga	cgttattgga	acagtggtag	tacttggttag	1553
cagcagtaat	aataatcatc	ataataaagc	tctgggttac	tgtcaaaaaa	aaaaaaaaaa	1613
aaaaa						1618

<210> 16

<211> 404

<212> PRT

<213> Oryza sativa

<400> 16

Met	Asp	Ser	Leu	Arg	Leu	Arg	Pro	Ser	Leu	Leu	Ala	Ala	Arg	Ala	Pro
1			5					10					15		
Gly	Ala	Ala	Ser	Leu	Pro	Pro	Leu	Arg	Asp	His	Phe	Leu	Pro	Pro	
			20					25				30			
Leu	Cys	Ser	Ile	His	Arg	Asn	Gly	Lys	Arg	Pro	Val	Ser	Leu	Ser	Ser
		35					40					45			
Gln	Arg	Thr	Gln	Gly	Pro	Ser	Phe	Asp	Gln	Cys	Gln	Lys	Phe	Phe	Gly
	50					55					60				
Trp	Lys	Ser	Ser	His	His	Arg	Ile	Pro	His	Arg	Pro	Thr	Ser	Ser	Ser
65					70					75					80
Ala	Asp	Ala	Ser	Gly	Gln	Pro	Leu	Gln	Ser	Ser	Ala	Glu	Ala	His	Asp
				85					90					95	
Ser	Ser	Ser	Ile	Trp	Lys	Pro	Ile	Ser	Ser	Ser	Pro	Asp	Ala	Phe	Tyr
			100					105					110		
Arg	Phe	Ser	Arg	Pro	His	Thr	Val	Ile	Gly	Thr	Ala	Leu	Ser	Ile	Val
		115					120					125			
Ser	Val	Ser	Leu	Leu	Ala	Val	Glu	Asn	Leu	Ser	Asp	Val	Ser	Pro	Leu
	130					135					140				
Phe	Leu	Thr	Gly	Leu	Leu	Glu	Ala	Val	Val	Ala	Ala	Leu	Phe	Met	Asn
145					150					155					160
Ile	Tyr	Ile	Val	Gly	Leu	Asn	Gln	Leu	Phe	Asp	Ile	Glu	Ile	Asp	Lys
			165						170					175	
Val	Asn	Lys	Pro	Thr	Leu	Pro	Leu	Ala	Ser	Gly	Glu	Tyr	Ser	Pro	Ala
			180					185					190		
Thr	Gly	Val	Ala	Leu	Val	Ser	Ala	Phe	Ala	Ala	Met	Ser	Phe	Gly	Leu
		195					200					205			
Gly	Trp	Ala	Val	Gly	Ser	Gln	Pro	Leu	Phe	Leu	Ala	Leu	Phe	Ile	Ser
	210					215					220				
Phe	Ile	Leu	Gly	Thr	Ala	Tyr	Ser	Ile	Asn	Leu	Pro	Phe	Leu	Arg	Trp
225					230					235					240
Lys	Arg	Ser	Ala	Val	Val	Ala	Ala	Leu	Cys	Ile	Leu	Ala	Val	Arg	Ala
			245						250					255	
Val	Ile	Val	Gln	Leu	Ala	Phe	Phe	Leu	His	Ile	Gln	Thr	Phe	Val	Phe
		260						265					270		
Arg	Arg	Pro	Ala	Val	Phe	Thr	Arg	Pro	Leu	Ile	Phe	Ala	Thr	Ala	Phe
		275					280					285			
Met	Thr	Phe	Phe	Ser	Val	Val	Ile	Ala	Leu	Phe	Lys	Asp	Ile	Pro	Asp
	290					295					300				
Ile	Glu	Gly	Asp	Arg	Ile	Phe	Gly	Ile	Lys	Ser	Phe	Ser	Val	Arg	Leu
305					310					315					320
Gly	Gln	Lys	Lys	Val	Phe	Trp	Ile	Cys	Val	Gly	Leu	Leu	Glu	Met	Ala
			325						330					335	
Tyr	Cys	Val	Ala	Ile	Leu	Met	Gly	Ala	Thr	Ser	Ala	Cys	Leu	Trp	Ser

			340						345					350					
Lys	Tyr	Ala	Thr	Val	Val	Gly	His	Ala	Ile	Leu	Ala	Ala	Ile	Leu	Trp				
		355					360					365							
Asn	Arg	Ser	Arg	Ser	Ile	Asp	Leu	Thr	Ser	Lys	Thr	Ala	Ile	Thr	Ser				
	370					375					380								
Phe	Tyr	Met	Phe	Ile	Trp	Lys	Leu	Phe	Tyr	Ala	Glu	Tyr	Leu	Leu	Ile				
385					390					395					400				
Pro	Leu	Val	Arg																

<210> 17
 <211> 1733
 <212> DNA
 <213> Oryza Sativa

<220>
 <221> CDS
 <222> (1)...(1137)

<400> 17	
ctt aca ctc gcc tcc cct cct ctc ccc tgc cgc gcc gcc gcc acc gcc	48
Leu Thr Leu Ala Ser Pro Pro Leu Pro Cys Arg Ala Ala Ala Thr Ala	
1 5 10 15	
agc cgc agc ggg cgt cct gct ccg cgc ctc ctc ggc cct ccg ccg ccg	96
Ser Arg Ser Gly Arg Pro Ala Pro Arg Leu Leu Gly Pro Pro Pro Pro	
20 25 30	
ccc gct tcc cct ctc ctc tcc tcc gct tcg gcg cgc ttc ccg cgt gcc	144
Pro Ala Ser Pro Leu Leu Ser Ser Ala Ser Ala Arg Phe Pro Arg Ala	
35 40 45	
ccc tgc aac gcc gca cgc tgg agc cgg cgc gac gcc gtg cgg gtt tgc	192
Pro Cys Asn Ala Ala Arg Trp Ser Arg Arg Asp Ala Val Arg Val Cys	
50 55 60	
tct caa gct ggt gca gct gga cca gcc cca tta tcg aag aca ttg tca	240
Ser Gln Ala Gly Ala Ala Gly Pro Ala Pro Leu Ser Lys Thr Leu Ser	
65 70 75 80	
gac ctc aag gat tcc tgc tgg aga ttt tta cgg cca cat aca att cga	288
Asp Leu Lys Asp Ser Cys Trp Arg Phe Leu Arg Pro His Thr Ile Arg	
85 90 95	
gga act gcc ttg gga tcc ata gca tta gtt gct aga gct ttg ata gag	336
Gly Thr Ala Leu Gly Ser Ile Ala Leu Val Ala Arg Ala Leu Ile Glu	
100 105 110	
aac ccc caa ctg ata aat tgg tgg ttg gta ttc aaa gcg ttc tat ggg	384
Asn Pro Gln Leu Ile Asn Trp Trp Leu Val Phe Lys Ala Phe Tyr Gly	
115 120 125	
ctc gtg gcg tta atc tgt ggc aat ggt tac atc gtt ggg atc aat cag	432
Leu Val Ala Leu Ile Cys Gly Asn Gly Tyr Ile Val Gly Ile Asn Gln	
130 135 140	
atc tat gac att aga atc gat aag gta aac aag cca tat tta cca att	480

Ile Tyr Asp Ile Arg Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Ile	
145 150 155 160	
gct gcc ggt gat ctc tca gtt cag aca gca tgg tta ttg gtg gta tta	528
Ala Ala Gly Asp Leu Ser Val Gln Thr Ala Trp Leu Leu Val Val Leu	
165 170 175	
ttt gca gct gcg gga ttt tca att gtt gtg aca aac ttt gga cct ttc	576
Phe Ala Ala Ala Gly Phe Ser Ile Val Val Thr Asn Phe Gly Pro Phe	
180 185 190	
att acc tct cta tat tgc ctt ggt cta ttt ctt ggc acc ata tac tct	624
Ile Thr Ser Leu Tyr Cys Leu Gly Leu Phe Leu Gly Thr Ile Tyr Ser	
195 200 205	
gtt cct cca ttc aga ctt aag aga tat cct gtt gct gct ttt ctt atc	672
Val Pro Pro Phe Arg Leu Lys Arg Tyr Pro Val Ala Ala Phe Leu Ile	
210 215 220	
att gca acg gtc cgt ggt ttt ctt ctc aac ttt ggt gtg tac tat gct	720
Ile Ala Thr Val Arg Gly Phe Leu Leu Asn Phe Gly Val Tyr Tyr Ala	
225 230 235 240	
act aga gca gca ctg ggt ctt aca ttc caa tgg agc tcg cct gtt gct	768
Thr Arg Ala Ala Leu Gly Leu Thr Phe Gln Trp Ser Ser Pro Val Ala	
245 250 255	
ttc att aca tgc ttc gtg act tta ttt gct ttg gtc att gct ata acc	816
Phe Ile Thr Cys Phe Val Thr Leu Phe Ala Leu Val Ile Ala Ile Thr	
260 265 270	
aaa gat ctc cca gat gtt gaa ggg gat cgg aag tat caa ata tca act	864
Lys Asp Leu Pro Asp Val Glu Gly Asp Arg Lys Tyr Gln Ile Ser Thr	
275 280 285	
ttg gcg aca aag ctc ggt gtc aga aac att gca ttt ctt ggc tct ggt	912
Leu Ala Thr Lys Leu Gly Val Arg Asn Ile Ala Phe Leu Gly Ser Gly	
290 295 300	
tta ttg ata gca aat tat gtt gct gct att gct gta gct ttt ctc atg	960
Leu Leu Ile Ala Asn Tyr Val Ala Ala Ile Ala Val Ala Phe Leu Met	
305 310 315 320	
cct cag gct ttc agg cgc act gta atg gtg cct gtg cat gct gcc ctt	1008
Pro Gln Ala Phe Arg Arg Thr Val Met Val Pro Val His Ala Ala Leu	
325 330 335	
gcc gtt ggt ata att ttc cag aca tgg gtt ctg gag caa gca aaa tat	1056
Ala Val Gly Ile Ile Phe Gln Thr Trp Val Leu Glu Gln Ala Lys Tyr	
340 345 350	
act aag gat gct att tca cag tac tac cgg ttc att tgg aat ctc ttc	1104
Thr Lys Asp Ala Ile Ser Gln Tyr Tyr Arg Phe Ile Trp Asn Leu Phe	
355 360 365	
tat gct gaa tac atc ttc ttc ccg ttg ata tag agaccaagca atctgatatg	1157
Tyr Ala Glu Tyr Ile Phe Phe Pro Leu Ile *	
370 375	

```

gtctgcatgt tgagtgcggc aaaaactaga agcccatatg aacagtggga gtaagggaac 1217
gaacatgcca tccatgggaa gactctgata actctctctc gcccgggctg taaagggtaa 1277
gcactgttgt gcatatatat gaaaggaagg tgataaagca gggatgctaa attgctactg 1337
ggatccttaa aggttatatg tggtcaccag tggaatgtgc cttaataatt tggttaccta 1397
gcagagcaag tttttgcagg ttattaggta atatctttga gggaatgaac ttagatttca 1457
ttgttttaag gtctggtcac acaacgggta gtagttctgg agcggcaaaa gacgacctg 1517
ttttacacta ccaagggagg ttaactctag ttttcatgtg accacttacc ttgagagttg 1577
agaccatgga atcacttgtc gactcctcgg cttgtatatt tctagtgtca gcatttgcac 1637
tctcctccac acttgtactt gaagagttga agacaacttt tttgtttgtg tatttctgga 1697
gtgtcagcat ttgcattcaa aaaaaaaaaa aaaaaa 1733

```

<210> 18

<211> 378

<212> PRT

<213> Oryza Sativa

<400> 18

```

Leu Thr Leu Ala Ser Pro Pro Leu Pro Cys Arg Ala Ala Ala Thr Ala
1          5          10          15
Ser Arg Ser Gly Arg Pro Ala Pro Arg Leu Leu Gly Pro Pro Pro Pro
20          25          30
Pro Ala Ser Pro Leu Leu Ser Ser Ala Ser Ala Arg Phe Pro Arg Ala
35          40          45
Pro Cys Asn Ala Ala Arg Trp Ser Arg Arg Asp Ala Val Arg Val Cys
50          55          60
Ser Gln Ala Gly Ala Ala Gly Pro Ala Pro Leu Ser Lys Thr Leu Ser
65          70          75          80
Asp Leu Lys Asp Ser Cys Trp Arg Phe Leu Arg Pro His Thr Ile Arg
85          90          95
Gly Thr Ala Leu Gly Ser Ile Ala Leu Val Ala Arg Ala Leu Ile Glu
100         105         110
Asn Pro Gln Leu Ile Asn Trp Trp Leu Val Phe Lys Ala Phe Tyr Gly
115         120         125
Leu Val Ala Leu Ile Cys Gly Asn Gly Tyr Ile Val Gly Ile Asn Gln
130         135         140
Ile Tyr Asp Ile Arg Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Ile
145         150         155         160
Ala Ala Gly Asp Leu Ser Val Gln Thr Ala Trp Leu Leu Val Val Leu
165         170         175
Phe Ala Ala Ala Gly Phe Ser Ile Val Val Thr Asn Phe Gly Pro Phe
180         185         190
Ile Thr Ser Leu Tyr Cys Leu Gly Leu Phe Leu Gly Thr Ile Tyr Ser
195         200         205
Val Pro Pro Phe Arg Leu Lys Arg Tyr Pro Val Ala Ala Phe Leu Ile
210         215         220
Ile Ala Thr Val Arg Gly Phe Leu Leu Asn Phe Gly Val Tyr Tyr Ala
225         230         235         240
Thr Arg Ala Ala Leu Gly Leu Thr Phe Gln Trp Ser Ser Pro Val Ala
245         250         255
Phe Ile Thr Cys Phe Val Thr Leu Phe Ala Leu Val Ile Ala Ile Thr
260         265         270
Lys Asp Leu Pro Asp Val Glu Gly Asp Arg Lys Tyr Gln Ile Ser Thr
275         280         285
Leu Ala Thr Lys Leu Gly Val Arg Asn Ile Ala Phe Leu Gly Ser Gly
290         295         300
Leu Leu Ile Ala Asn Tyr Val Ala Ala Ile Ala Val Ala Phe Leu Met
305         310         315         320

```

Pro	Gln	Ala	Phe	Arg	Arg	Thr	Val	Met	Val	Pro	Val	His	Ala	Ala	Leu
				325					330					335	
Ala	Val	Gly	Ile	Ile	Phe	Gln	Thr	Trp	Val	Leu	Glu	Gln	Ala	Lys	Tyr
			340					345					350		
Thr	Lys	Asp	Ala	Ile	Ser	Gln	Tyr	Tyr	Arg	Phe	Ile	Trp	Asn	Leu	Phe
		355					360					365			
Tyr	Ala	Glu	Tyr	Ile	Phe	Phe	Pro	Leu	Ile						
	370					375									

<210> 19
 <211> 1400
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (37)...(1203)

<400> 19	
ctgcagggtt ttttcgtttg ctgtgttcag ctcctt atg gag ctc tca ctc tct	54
Met Glu Leu Ser Leu Ser	
1 5	
cca act tca cat cgt gtt cct tcc aca att ccc act ttg aat ttc gct	102
Pro Thr Ser His Arg Val Pro Ser Thr Ile Pro Thr Leu Asn Phe Ala	
10 15 20	
aaa cta tca ttc act aag gcc aca acg tcc caa cct ttg ttc tta gga	150
Lys Leu Ser Phe Thr Lys Ala Thr Thr Ser Gln Pro Leu Phe Leu Gly	
25 30 35	
ttt tcc aaa cac ttc aac tca att ggg ttg aac cat cac agt tac aga	198
Phe Ser Lys His Phe Asn Ser Ile Gly Leu Asn His His Ser Tyr Arg	
40 45 50	
tgc tgc tca aat gct gtt cct aag aga ccc caa aga ccc agt tcc ata	246
Cys Cys Ser Asn Ala Val Pro Lys Arg Pro Gln Arg Pro Ser Ser Ile	
55 60 65 70	
agg gcc tgc act gga gtt gga gct gct ggt tct gat cgt cca tta gct	294
Arg Ala Cys Thr Gly Val Gly Ala Ala Gly Ser Asp Arg Pro Leu Ala	
75 80 85	
gaa aga ctt tta gat ttg aaa gat gct tgc tgg aga ttt tta agg cca	342
Glu Arg Leu Leu Asp Leu Lys Asp Ala Cys Trp Arg Phe Leu Arg Pro	
90 95 100	
cat act ata cgt ggt aca gca cta ggt tca ttt gct ttg gtg gca aga	390
His Thr Ile Arg Gly Thr Ala Leu Gly Ser Phe Ala Leu Val Ala Arg	
105 110 115	
gca ttg att gag aac acg aat ttg ata aag tgg tct ctt ttg ttc aaa	438
Ala Leu Ile Glu Asn Thr Asn Leu Ile Lys Trp Ser Leu Leu Phe Lys	
120 125 130	
gct ttc tct ggt ctt ttt gcc ctg att tgt ggg aat ggt tat ata gtt	486
Ala Phe Ser Gly Leu Phe Ala Leu Ile Cys Gly Asn Gly Tyr Ile Val	

135	140	145	150	
ggc atc aat caa atc tat gac att agc att gac aag gta aac aaa cct				534
Gly Ile Asn Gln Ile Tyr Asp Ile Ser Ile Asp Lys Val Asn Lys Pro	155	160	165	
tat tta cct ata gct gct gga gat ctt tct gtc caa tct gca tgg ttc				582
Tyr Leu Pro Ile Ala Ala Gly Asp Leu Ser Val Gln Ser Ala Trp Phe	170	175	180	
ttg gtt ata ttt ttt gca gca gct ggc ctg tcg att gca ggg ttg aac				630
Leu Val Ile Phe Phe Ala Ala Ala Gly Leu Ser Ile Ala Gly Leu Asn	185	190	195	
ttt ggg cct ttc att ttt tct ctt tac aca ctt ggc ctt ttc ttg gga				678
Phe Gly Pro Phe Ile Phe Ser Leu Tyr Thr Leu Gly Leu Phe Leu Gly	200	205	210	
acc atc tat tct gtt cct cca ttg agg atg aaa cgc ttt cct gtt gca				726
Thr Ile Tyr Ser Val Pro Pro Leu Arg Met Lys Arg Phe Pro Val Ala	215	220	225	230
gca ttt ctt ata att gcc acg gta cgt ggt ttt ctc ctt aac ttt ggt				774
Ala Phe Leu Ile Ile Ala Thr Val Arg Gly Phe Leu Leu Asn Phe Gly	235	240	245	
gtg tac tat gcc act aga gct tcc ctt ggg ctt gca ttt gaa tgg agc				822
Val Tyr Tyr Ala Thr Arg Ala Ser Leu Gly Leu Ala Phe Glu Trp Ser	250	255	260	
tct cct gtg gtt ttt atc aca aca ttt gta aca ttt ttc gca ctg gta				870
Ser Pro Val Val Phe Ile Thr Thr Phe Val Thr Phe Phe Ala Leu Val	265	270	275	
att gct ata aca aaa gat ctt cct gat gtt gaa ggt gat cgc aag tat				918
Ile Ala Ile Thr Lys Asp Leu Pro Asp Val Glu Gly Asp Arg Lys Tyr	280	285	290	
cag ata tca acc ttt gct aca aaa tta gga gtt cgg aac att gct ttc				966
Gln Ile Ser Thr Phe Ala Thr Lys Leu Gly Val Arg Asn Ile Ala Phe	295	300	305	310
ctt ggt tct gga att ttg ctg gtg aat tat att gtt tct gtt ttg gca				1014
Leu Gly Ser Gly Ile Leu Leu Val Asn Tyr Ile Val Ser Val Leu Ala	315	320	325	
gca att tat atg cct cag gct ttc agg cgt tgg tta ctc ata cca gct				1062
Ala Ile Tyr Met Pro Gln Ala Phe Arg Arg Trp Leu Leu Ile Pro Ala	330	335	340	
cat aca att ttt gca ata agc ttg att tac cag gca cga ata tta gaa				1110
His Thr Ile Phe Ala Ile Ser Leu Ile Tyr Gln Ala Arg Ile Leu Glu	345	350	355	
caa gca aat tat acc aag gat gca ata tca gga ttc tat cga ttc ata				1158
Gln Ala Asn Tyr Thr Lys Asp Ala Ile Ser Gly Phe Tyr Arg Phe Ile	360	365	370	

tgg	aat	ctg	ttc	tat	gct	gag	tat	gca	ata	ttt	cct	ttc	ata	tag		1203
Trp	Asn	Leu	Phe	Tyr	Ala	Glu	Tyr	Ala	Ile	Phe	Pro	Phe	Ile	*		
375					380					385						

caaaccttgc	tacttttttc	ttgggaaaag	gtgcatacgt	gcatagttag	agagatcttt	1263
gtttatcaag	tgtcaattgg	taaactagct	atcattattt	ttttaaaatg	agtattgttg	1323
tatataaatg	tgatactatt	tcctttttact	ttgacgtaat	gccattaaca	tattttcataa	1383
aaaaaaaaaa	aaaaaaa					1400

```
<210> 20
<211> 388
<212> PRT
<213> Glycine max
```

<400> 20															
Met 1	Glu	Leu	Ser	Leu 5	Ser	Pro	Thr	Ser	His 10	Arg	Val	Pro	Ser	Thr 15	Ile
Pro	Thr	Leu	Asn 20	Phe	Ala	Lys	Leu	Ser 25	Phe	Thr	Lys	Ala	Thr 30	Thr	Ser
Gln	Pro	Leu	Phe	Leu	Gly	Phe	Ser 40	Lys	His	Phe	Asn	Ser 45	Ile	Gly	Leu
Asn	His 50	His	Ser	Tyr	Arg	Cys 55	Cys	Ser	Asn	Ala	Val 60	Pro	Lys	Arg	Pro
Gln 65	Arg	Pro	Ser	Ser	Ile 70	Arg	Ala	Cys	Thr	Gly 75	Val	Gly	Ala	Ala	Gly 80
Ser	Asp	Arg	Pro	Leu 85	Ala	Glu	Arg	Leu	Leu 90	Asp	Leu	Lys	Asp	Ala	Cys 95
Trp	Arg	Phe	Leu 100	Arg	Pro	His	Thr	Ile 105	Arg	Gly	Thr	Ala	Leu 110	Gly	Ser
Phe	Ala	Leu	Val	Ala	Arg	Ala	Leu 120	Ile	Glu	Asn	Thr	Asn	Leu 125	Ile	Lys
Trp	Ser	Leu	Leu	Phe	Lys	Ala	Phe 135	Ser	Gly	Leu	Phe	Ala	Leu	Ile	Cys
Gly 145	Asn	Gly	Tyr	Ile	Val 150	Gly	Ile	Asn	Gln	Ile	Tyr	Asp	Ile	Ser	Ile 160
Asp	Lys	Val	Asn	Lys 165	Pro	Tyr	Leu	Pro	Ile 170	Ala	Ala	Gly	Asp	Leu 175	Ser
Val	Gln	Ser	Ala	Trp 180	Phe	Leu	Val	Ile 185	Phe	Phe	Ala	Ala	Ala	Gly	Leu
Ser	Ile	Ala	Gly	Leu	Asn	Phe	Gly 200	Pro	Phe	Ile	Phe	Ser	Leu	Tyr	Thr
Leu	Gly 210	Leu	Phe	Leu	Gly	Thr 215	Ile	Tyr	Ser	Val	Pro	Pro	Leu	Arg	Met
Lys 225	Arg	Phe	Pro	Val	Ala	Ala	Phe	Leu	Ile	Ile	Ala	Thr	Val	Arg	Gly 240
Phe	Leu	Leu	Asn	Phe	Gly	Val	Tyr	Tyr	Ala	Thr	Arg	Ala	Ser	Leu	Gly
Leu	Ala	Phe	Glu	Trp	Ser	Ser	Pro	Val	Val	Phe	Ile	Thr	Thr	Phe	Val
Thr	Phe	Phe	Ala	Leu	Val	Ile	Ala	Ile	Thr	Lys	Asp	Leu	Pro	Asp	Val
Glu	Gly 290	Asp	Arg	Lys	Tyr	Gln	Ile	Ser	Thr	Phe	Ala	Thr	Lys	Leu	Gly
Val 305	Arg	Asn	Ile	Ala	Phe	Leu	Gly	Ser	Gly	Ile	Leu	Leu	Val	Asn	Tyr
Ile	Val	Ser	Val	Leu	Ala	Ala	Ile	Tyr	Met	Pro	Gln	Ala	Phe	Arg	Arg
Trp	Leu	Leu	Ile	Pro	Ala	His	Thr	Ile	Phe	Ala	Ile	Ser	Leu	Ile	Tyr

	340		345		350										
Gln	Ala	Arg	Ile	Leu	Glu	Gln	Ala	Asn	Tyr	Thr	Lys	Asp	Ala	Ile	Ser
	355		360		365										
Gly	Phe	Tyr	Arg	Phe	Ile	Trp	Asn	Leu	Phe	Tyr	Ala	Glu	Tyr	Ala	Ile
	370		375		380										
Phe	Pro	Phe	Ile												
385															

<210> 21
 <211> 1370
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (24)...(1211)

<400> 21	
gcacgagagc actactgtta tat atg gat tcg atg ctt ctt cga tct ttt cct	53
Met Asp Ser Met Leu Leu Arg Ser Phe Pro	
1 5 10	
aat att aac aac gct tct tct ctc gcc acc act ggt tct tat ttg cca	101
Asn Ile Asn Asn Ala Ser Ser Leu Ala Thr Thr Gly Ser Tyr Leu Pro	
15 20 25	
aat gct tca tgg cac aat agg aaa atc caa aaa gaa tat aat ttt ttg	149
Asn Ala Ser Trp His Asn Arg Lys Ile Gln Lys Glu Tyr Asn Phe Leu	
30 35 40	
agg ttt cgg tgg cca agt ttg aac cac cat tac aaa agc att gaa gga	197
Arg Phe Arg Trp Pro Ser Leu Asn His His Tyr Lys Ser Ile Glu Gly	
45 50 55	
ggg tgt aca tgt aaa aaa tgt aat ata aaa ttt gtt gtg aaa gcg acc	245
Gly Cys Thr Cys Lys Lys Cys Asn Ile Lys Phe Val Val Lys Ala Thr	
60 65 70	
tct gaa aaa tct ttt gag tct gaa cct caa gct ttt gat cca aaa agc	293
Ser Glu Lys Ser Phe Glu Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser	
75 80 85 90	
att ttg gac tct gtc aag aat tcc ttg gat gct ttc tac agg ttt tcc	341
Ile Leu Asp Ser Val Lys Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser	
95 100 105	
aga cct cac aca gtt att ggc aca gca tta agc ata att tct gtg tcc	389
Arg Pro His Thr Val Ile Gly Thr Ala Leu Ser Ile Ile Ser Val Ser	
110 115 120	
ctc ctt gct gtt gag aaa ata tca gat ata tct cca tta ttt ttt act	437
Leu Leu Ala Val Glu Lys Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr	
125 130 135	
ggg gtg ttg gag gct gtg gtt gct gcc ctg ttt atg aat att tat att	485
Gly Val Leu Glu Ala Val Val Ala Ala Leu Phe Met Asn Ile Tyr Ile	
140 145 150	

gtt ggt ttg aat caa ttg tct gat gtt gaa ata gac aag ata aac aag	533
Val Gly Leu Asn Gln Leu Ser Asp Val Glu Ile Asp Lys Ile Asn Lys	
155 160 165 170	
ccg tat ctt cca tta gca tct ggg gaa tat tcc ttt gaa act ggt gtc	581
Pro Tyr Leu Pro Leu Ala Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val	
175 180 185	
act att gtt gca tct ttt tca att ctg agt ttt tgg ctt ggc tgg gtt	629
Thr Ile Val Ala Ser Phe Ser Ile Leu Ser Phe Trp Leu Gly Trp Val	
190 195 200	
gta ggt tca tgg cca tta ttt tgg gcc ctt ttt gta agc ttt gtg cta	677
Val Gly Ser Trp Pro Leu Phe Trp Ala Leu Phe Val Ser Phe Val Leu	
205 210 215	
gga act gct tat tca atc aat gtg cct ctg ttg aga tgg aag agg ttt	725
Gly Thr Ala Tyr Ser Ile Asn Val Pro Leu Leu Arg Trp Lys Arg Phe	
220 225 230	
gca gtg ctt gca gcg atg tgc att cta gct gtt cgg gca gta ata gtt	773
Ala Val Leu Ala Ala Met Cys Ile Leu Ala Val Arg Ala Val Ile Val	
235 240 245 250	
caa ctt gca ttt ttc ctt cac atc cag act cat gta tac aag agg cca	821
Gln Leu Ala Phe Phe Leu His Ile Gln Thr His Val Tyr Lys Arg Pro	
255 260 265	
cct gtc ttt tca aga tca ttg att ttt gct act gca ttc atg agc ttc	869
Pro Val Phe Ser Arg Ser Leu Ile Phe Ala Thr Ala Phe Met Ser Phe	
270 275 280	
ttc tct gta gtt ata gca ctg ttt aag gat ata cct gac att gaa gga	917
Phe Ser Val Val Ile Ala Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly	
285 290 295	
gat aaa gta ttt ggc atc caa tct ttt tca gtg cgt tta ggt cag aag	965
Asp Lys Val Phe Gly Ile Gln Ser Phe Ser Val Arg Leu Gly Gln Lys	
300 305 310	
ccg gta ttc tgg act tgt gtt atc ctt ctt gaa ata gct tat gga gtc	1013
Pro Val Phe Trp Thr Cys Val Ile Leu Leu Glu Ile Ala Tyr Gly Val	
315 320 325 330	
gcc ctc ctg gtg gga gct gca tct cct tgt ctt tgg agc aaa att gtc	1061
Ala Leu Leu Val Gly Ala Ala Ser Pro Cys Leu Trp Ser Lys Ile Val	
335 340 345	
acg ggt ctg gga cac gct gtt ctg gct tca att ctc tgg ttt cat gcc	1109
Thr Gly Leu Gly His Ala Val Leu Ala Ser Ile Leu Trp Phe His Ala	
350 355 360	
aaa tct gta gat ttg aaa agc aaa gct tcg ata aca tcc ttc tat atg	1157
Lys Ser Val Asp Leu Lys Ser Lys Ala Ser Ile Thr Ser Phe Tyr Met	
365 370 375	
ttt att tgg aag cta ttt tat gca gaa tac tta ctc att cct ttt gtt	1205

Phe Ile Trp Lys Leu Phe Tyr Ala Glu Tyr Leu Leu Ile Pro Phe Val
 380 385 390

aga tga ggatgcagcg gcaatattga cttgagaatt agttttgttt aaatgggtgct 1261
 Arg *
 395

gcctttgtca caggccggct tggagtcgct acattagttt taagttttta attgctaatt 1321
 taaatgaaga tatatttctt ttgggatgaa aaaaaaaaaa aaaaaaaaaa 1370

<210> 22
 <211> 395
 <212> PRT
 <213> Glycine max

<400> 22
 Met Asp Ser Met Leu Leu Arg Ser Phe Pro Asn Ile Asn Asn Ala Ser
 1 5 10 15
 Ser Leu Ala Thr Gly Ser Tyr Leu Pro Asn Ala Ser Trp His Asn
 20 25 30
 Arg Lys Ile Gln Lys Glu Tyr Asn Phe Leu Arg Phe Arg Trp Pro Ser
 35 40 45
 Leu Asn His His Tyr Lys Ser Ile Glu Gly Gly Cys Thr Cys Lys Lys
 50 55 60
 Cys Asn Ile Lys Phe Val Val Lys Ala Thr Ser Glu Lys Ser Phe Glu
 65 70 75 80
 Ser Glu Pro Gln Ala Phe Asp Pro Lys Ser Ile Leu Asp Ser Val Lys
 85 90 95
 Asn Ser Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile
 100 105 110
 Gly Thr Ala Leu Ser Ile Ile Ser Val Ser Leu Leu Ala Val Glu Lys
 115 120 125
 Ile Ser Asp Ile Ser Pro Leu Phe Phe Thr Gly Val Leu Glu Ala Val
 130 135 140
 Val Ala Ala Leu Phe Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu
 145 150 155 160
 Ser Asp Val Glu Ile Asp Lys Ile Asn Lys Pro Tyr Leu Pro Leu Ala
 165 170 175
 Ser Gly Glu Tyr Ser Phe Glu Thr Gly Val Thr Ile Val Ala Ser Phe
 180 185 190
 Ser Ile Leu Ser Phe Trp Leu Gly Trp Val Val Gly Ser Trp Pro Leu
 195 200 205
 Phe Trp Ala Leu Phe Val Ser Phe Val Leu Gly Thr Ala Tyr Ser Ile
 210 215 220
 Asn Val Pro Leu Leu Arg Trp Lys Arg Phe Ala Val Leu Ala Ala Met
 225 230 235 240
 Cys Ile Leu Ala Val Arg Ala Val Ile Val Gln Leu Ala Phe Phe Leu
 245 250 255
 His Ile Gln Thr His Val Tyr Lys Arg Pro Pro Val Phe Ser Arg Ser
 260 265 270
 Leu Ile Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala
 275 280 285
 Leu Phe Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Val Phe Gly Ile
 290 295 300
 Gln Ser Phe Ser Val Arg Leu Gly Gln Lys Pro Val Phe Trp Thr Cys
 305 310 315 320
 Val Ile Leu Leu Glu Ile Ala Tyr Gly Val Ala Leu Leu Val Gly Ala
 325 330 335

Ala	Ser	Pro	Cys	Leu	Trp	Ser	Lys	Ile	Val	Thr	Gly	Leu	Gly	His	Ala
			340					345					350		
Val	Leu	Ala	Ser	Ile	Leu	Trp	Phe	His	Ala	Lys	Ser	Val	Asp	Leu	Lys
		355					360					365			
Ser	Lys	Ala	Ser	Ile	Thr	Ser	Phe	Tyr	Met	Phe	Ile	Trp	Lys	Leu	Phe
	370					375					380				
Tyr	Ala	Glu	Tyr	Leu	Leu	Ile	Pro	Phe	Val	Arg					
385					390					395					

<210> 23
 <211> 1575
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (109)...(1338)

<400> 23															
cgaggagaga	gagagaacta	gtctcgagtt	tagtctctac	aatcactcct	tcctctcatc										60
ctctataaag	aaagtgccta	atttgtgttg	ttacttggtt	cagtttcc	atg gat tgg										117
					Met Asp Trp										
					1										
ggg ctt gct ata tct tct cat cct aaa cct tat tca gtc aca act ggt															165
Gly Leu Ala Ile Ser Ser His Pro Lys Pro Tyr Ser Val Thr Thr Gly															
5					10					15					
gga aat ctc tgg cgg agt aaa cac acc acc aag aat att tac ttt gca															213
Gly Asn Leu Trp Arg Ser Lys His Thr Thr Lys Asn Ile Tyr Phe Ala															
20				25					30					35	
agt tct tgg ata tca aaa gct tca cga cac aaa agg gaa act caa ata															261
Ser Ser Trp Ile Ser Lys Ala Ser Arg His Lys Arg Glu Thr Gln Ile															
			40				45							50	
gaa cat aat gtt ttg agg ttc caa caa cca agt ttg gat cat cat tac															309
Glu His Asn Val Leu Arg Phe Gln Gln Pro Ser Leu Asp His His Tyr															
			55				60						65		
aaa tgc atc aga gga ggg tct aca tat caa gaa tgc aat aga aaa ttt															357
Lys Cys Ile Arg Gly Gly Ser Thr Tyr Gln Glu Cys Asn Arg Lys Phe															
		70				75						80			
gtt gtg aag gca atc tct aaa caa cct ctt ggt ttt gaa gct cat gct															405
Val Val Lys Ala Ile Ser Lys Gln Pro Leu Gly Phe Glu Ala His Ala															
		85				90						95			
tcc aat cct aag aac att ttg gac tct gtc aaa aat gta ttg tct gct															453
Ser Asn Pro Lys Asn Ile Leu Asp Ser Val Lys Asn Val Leu Ser Ala															
100					105					110				115	
ttc tac tgg ttt tcc tat cca tac aca atg att ggc ata aca tta tgc															501
Phe Tyr Trp Phe Ser Tyr Pro Tyr Thr Met Ile Gly Ile Thr Leu Cys															
			120						125					130	
gca ttt tct tca tct ctt ctc gcg gtg gaa aaa tta tca gat ata tct															549

Ala Phe Ser Ser Ser Leu Leu Ala Val Glu Lys Leu Ser Asp Ile Ser	
135 140 145	
tta tca ttt tta att ggc gtg tta cag ggt gtg ctg cct caa ttg ttt	597
Leu Ser Phe Leu Ile Gly Val Leu Gln Gly Val Leu Pro Gln Leu Phe	
150 155 160	
att gaa att tat ctt tgt ggt gtg aat caa ctg tat gac ctt gaa ata	645
Ile Glu Ile Tyr Leu Cys Gly Val Asn Gln Leu Tyr Asp Leu Glu Ile	
165 170 175	
gac aag ata aac aaa cca cat ctt cca atg gca tct gga caa ttt tcc	693
Asp Lys Ile Asn Lys Pro His Leu Pro Met Ala Ser Gly Gln Phe Ser	
180 185 190 195	
ttt aaa acc ggt gtc att att tct gca gca ttt tta gct ctg agt ttt	741
Phe Lys Thr Gly Val Ile Ile Ser Ala Ala Phe Leu Ala Leu Ser Phe	
200 205 210	
gga ttt act tgg att acc ggc tct tgg cca ttg att tgt aat ctt gta	789
Gly Phe Thr Trp Ile Thr Gly Ser Trp Pro Leu Ile Cys Asn Leu Val	
215 220 225	
gta atc gct tca tcg tgg acg gct tat tca atc gat gtg ccc cta ctg	837
Val Ile Ala Ser Ser Trp Thr Ala Tyr Ser Ile Asp Val Pro Leu Leu	
230 235 240	
aga tgg aag aga tac cca ttt gtc gca gca atg tgc atg att tct act	885
Arg Trp Lys Arg Tyr Pro Phe Val Ala Ala Met Cys Met Ile Ser Thr	
245 250 255	
tgg gct ctt gca ttg cca att tca tat ttc cat cac atg cag acc gtt	933
Trp Ala Leu Ala Leu Pro Ile Ser Tyr Phe His His Met Gln Thr Val	
260 265 270 275	
gtg ttg aag agg cca att ggc ttt cca aga tca ttg ggt ttt ctt gtt	981
Val Leu Lys Arg Pro Ile Gly Phe Pro Arg Ser Leu Gly Phe Leu Val	
280 285 290	
gca ttc atg acc ttc tac tcc ttg ggt ttg gca ttg tcc aag gat ata	1029
Ala Phe Met Thr Phe Tyr Ser Leu Gly Leu Ala Leu Ser Lys Asp Ile	
295 300 305	
cct gac gtt gaa gga gat aaa gag cac ggc att gat tct ttt gca gta	1077
Pro Asp Val Glu Gly Asp Lys Glu His Gly Ile Asp Ser Phe Ala Val	
310 315 320	
cgt cta ggt cag aaa cgg gca ttt tgg att tgc gtt tcc ttt ttt gaa	1125
Arg Leu Gly Gln Lys Arg Ala Phe Trp Ile Cys Val Ser Phe Phe Glu	
325 330 335	
atg gct ttc gga gtt ggt atc ctg gcc gga gca tca tgc tca cac ttt	1173
Met Ala Phe Gly Val Gly Ile Leu Ala Gly Ala Ser Cys Ser His Phe	
340 345 350 355	
tgg act aaa att ttc acg ggt atg gga aat gct gtt ctt gct tca att	1221
Trp Thr Lys Ile Phe Thr Gly Met Gly Asn Ala Val Leu Ala Ser Ile	
360 365 370	

ctc tgg tac caa gcc aag tcc gta gat ttg agc gac aaa gct tcc act	1269
Leu Trp Tyr Gln Ala Lys Ser Val Asp Leu Ser Asp Lys Ala Ser Thr	
375 380 385	

gga tct ttc tat atg ttc atc tgg aag cta ttg tat gca ggg ttc ttt	1317
Gly Ser Phe Tyr Met Phe Ile Trp Lys Leu Leu Tyr Ala Gly Phe Phe	
390 395 400	

ctc atg gca tta att aga tga ggatatacgtg gaaggcttaa acaatgttct	1368
Leu Met Ala Leu Ile Arg *	
405	

cgacacatac accaaaataa aaggaatata tgttttgcat ctaagattta ttaaataaag	1428
ccgaatgttg gttcttgtat cattaagatt ttttttttaa ttgtcgaaga ctttatgtat	1488
tcatattcac cttgacttct acggtcaaat ttttcataaa gtggaataaa agcaacttgg	1548
tatacaaaaa aaaaaaaaaa aaaaaaa	1575

<210> 24

<211> 409

<212> PRT

<213> Glycine max

<400> 24

Met Asp Trp Gly Leu Ala Ile Ser Ser His Pro Lys Pro Tyr Ser Val	
1 5 10 15	
Thr Thr Gly Gly Asn Leu Trp Arg Ser Lys His Thr Thr Lys Asn Ile	
20 25 30	
Tyr Phe Ala Ser Ser Trp Ile Ser Lys Ala Ser Arg His Lys Arg Glu	
35 40 45	
Thr Gln Ile Glu His Asn Val Leu Arg Phe Gln Gln Pro Ser Leu Asp	
50 55 60	
His His Tyr Lys Cys Ile Arg Gly Gly Ser Thr Tyr Gln Glu Cys Asn	
65 70 75 80	
Arg Lys Phe Val Val Lys Ala Ile Ser Lys Gln Pro Leu Gly Phe Glu	
85 90 95	
Ala His Ala Ser Asn Pro Lys Asn Ile Leu Asp Ser Val Lys Asn Val	
100 105 110	
Leu Ser Ala Phe Tyr Trp Phe Ser Tyr Pro Tyr Thr Met Ile Gly Ile	
115 120 125	
Thr Leu Cys Ala Phe Ser Ser Ser Leu Leu Ala Val Glu Lys Leu Ser	
130 135 140	
Asp Ile Ser Leu Ser Phe Leu Ile Gly Val Leu Gln Gly Val Leu Pro	
145 150 155 160	
Gln Leu Phe Ile Glu Ile Tyr Leu Cys Gly Val Asn Gln Leu Tyr Asp	
165 170 175	
Leu Glu Ile Asp Lys Ile Asn Lys Pro His Leu Pro Met Ala Ser Gly	
180 185 190	
Gln Phe Ser Phe Lys Thr Gly Val Ile Ile Ser Ala Ala Phe Leu Ala	
195 200 205	
Leu Ser Phe Gly Phe Thr Trp Ile Thr Gly Ser Trp Pro Leu Ile Cys	
210 215 220	
Asn Leu Val Val Ile Ala Ser Ser Trp Thr Ala Tyr Ser Ile Asp Val	
225 230 235 240	
Pro Leu Leu Arg Trp Lys Arg Tyr Pro Phe Val Ala Ala Met Cys Met	
245 250 255	
Ile Ser Thr Trp Ala Leu Ala Leu Pro Ile Ser Tyr Phe His His Met	
260 265 270	

Gln Thr Val Val Leu Lys Arg Pro Ile Gly Phe Pro Arg Ser Leu Gly
 275 280 285
 Phe Leu Val Ala Phe Met Thr Phe Tyr Ser Leu Gly Leu Ala Leu Ser
 290 295 300
 Lys Asp Ile Pro Asp Val Glu Gly Asp Lys Glu His Gly Ile Asp Ser
 305 310 315 320
 Phe Ala Val Arg Leu Gly Gln Lys Arg Ala Phe Trp Ile Cys Val Ser
 325 330 335
 Phe Phe Glu Met Ala Phe Gly Val Gly Ile Leu Ala Gly Ala Ser Cys
 340 345 350
 Ser His Phe Trp Thr Lys Ile Phe Thr Gly Met Gly Asn Ala Val Leu
 355 360 365
 Ala Ser Ile Leu Trp Tyr Gln Ala Lys Ser Val Asp Leu Ser Asp Lys
 370 375 380
 Ala Ser Thr Gly Ser Phe Tyr Met Phe Ile Trp Lys Leu Leu Tyr Ala
 385 390 395 400
 Gly Phe Phe Leu Met Ala Leu Ile Arg
 405

<210> 25
 <211> 368
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)...(363)

<400> 25
 gca aca ttg ttc atg tgt tgc ttc tct gcc gtc ata gct cta ttc aag 48
 Ala Thr Leu Phe Met Cys Cys Phe Ser Ala Val Ile Ala Leu Phe Lys
 1 5 10 15
 gat att cct gat gtt gat gga gac cga gat ttt ggc atc caa tcc ttg 96
 Asp Ile Pro Asp Val Asp Gly Asp Arg Asp Phe Gly Ile Gln Ser Leu
 20 25 30
 agt gtg aga ttg ggg cca caa aga gtg tat cag ctc tgc ata agc ata 144
 Ser Val Arg Leu Gly Pro Gln Arg Val Tyr Gln Leu Cys Ile Ser Ile
 35 40 45
 ctg tta aca gcc tat ggg gct gcc act gta gta gga gct tca tcc aca 192
 Leu Leu Thr Ala Tyr Gly Ala Ala Thr Val Val Gly Ala Ser Ser Thr
 50 55 60
 cac cta ctt caa aag atc atc act gtg tct ggc cat ggc ctg ctt gct 240
 His Leu Leu Gln Lys Ile Ile Thr Val Ser Gly His Gly Leu Leu Ala
 65 70 75 80
 gtg aca ctt tgg cag aga gcg cgg cac ctt gag gtt gaa aac caa gcg 288
 Val Thr Leu Trp Gln Arg Ala Arg His Leu Glu Val Glu Asn Gln Ala
 85 90 95
 cgt gtc aca tca ttt tac atg ttc att tgg aag cta ttc tat gca aag 336
 Arg Val Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Lys
 100 105 110

tat ttc ctt ata ccg ttt gtg caa taa aattt
 Tyr Phe Leu Ile Pro Phe Val Gln *
 115 120

368

<210> 26
 <211> 120
 <212> PRT
 <213> Triticum aestivum

<400> 26
 Ala Thr Leu Phe Met Cys Cys Phe Ser Ala Val Ile Ala Leu Phe Lys
 1 5 10 15
 Asp Ile Pro Asp Val Asp Gly Asp Arg Asp Phe Gly Ile Gln Ser Leu
 20 25 30
 Ser Val Arg Leu Gly Pro Gln Arg Val Tyr Gln Leu Cys Ile Ser Ile
 35 40 45
 Leu Leu Thr Ala Tyr Gly Ala Ala Thr Val Val Gly Ala Ser Ser Thr
 50 55 60
 His Leu Leu Gln Lys Ile Ile Thr Val Ser Gly His Gly Leu Leu Ala
 65 70 75 80
 Val Thr Leu Trp Gln Arg Ala Arg His Leu Glu Val Glu Asn Gln Ala
 85 90 95
 Arg Val Thr Ser Phe Tyr Met Phe Ile Trp Lys Leu Phe Tyr Ala Lys
 100 105 110
 Tyr Phe Leu Ile Pro Phe Val Gln
 115 120

<210> 27
 <211> 1477
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (20)...(1171)

<400> 27
 cacgagcccc tccccaccc atg gct tcc ctc gcc tcc cct ccc gtc ccc tcc 52
 Met Ala Ser Leu Ala Ser Pro Pro Val Pro Ser
 1 5 10
 cac gcg ccc acc acc gcc gct cgc ttc ctc ccc gcg ccg gcc ggc cgc 100
 His Ala Pro Thr Thr Ala Ala Arg Phe Leu Pro Ala Pro Ala Gly Arg
 15 20 25
 ggc agg cgc ccg tcg ccg ccg gcc gct tca cct atc ttc tcc tct gct 148
 Gly Arg Arg Pro Ser Pro Pro Ala Ala Ser Pro Ile Phe Ser Ser Ala
 30 35 40
 tcc acc cga ttc acc cag tcc ccg cgc gcc ccc tgc ggc gcc gcc cga 196
 Ser Thr Arg Phe Thr Gln Ser Pro Arg Ala Pro Cys Gly Ala Ala Arg
 45 50 55
 ccg cgc tgg cgc gac acc gtg cgg gca tgc tct caa gct ggt gca gct 244
 Pro Arg Trp Arg Asp Thr Val Arg Ala Cys Ser Gln Ala Gly Ala Ala
 60 65 70 75

ggg cca gct cca ctg tca aag aca tta tca gac cta aag gat tcc tgc	292
Gly Pro Ala Pro Leu Ser Lys Thr Leu Ser Asp Leu Lys Asp Ser Cys	
80 85 90	
ttg aga ttt tta agg cca cac aca att cgt gga act gct ttg gga tcc	340
Trp Arg Phe Leu Arg Pro His Thr Ile Arg Gly Thr Ala Leu Gly Ser	
95 100 105	
aca gcc ttg gtt gct aga gca tta tta gag aat ccc caa ttg atc gat	388
Thr Ala Leu Val Ala Arg Ala Leu Leu Glu Asn Pro Gln Leu Ile Asp	
110 115 120	
ttg cgc ttg gta ttc aaa gca tta tat ggc ctt gta gct ttg atc tgc	436
Trp Arg Leu Val Phe Lys Ala Leu Tyr Gly Leu Val Ala Leu Ile Cys	
125 130 135	
ggc aac ggt tac att gtt ggg att aat cag atc tat gac att gga att	484
Gly Asn Gly Tyr Ile Val Gly Ile Asn Gln Ile Tyr Asp Ile Gly Ile	
140 145 150 155	
gac aag gta aac aaa cca tat tta cct att gct gcc ggt gat ctc tca	532
Asp Lys Val Asn Lys Pro Tyr Leu Pro Ile Ala Ala Gly Asp Leu Ser	
160 165 170	
gtt cag tca gca tgg tta ctg gtc gta gca ttc gca gtg gtg ggc ttc	580
Val Gln Ser Ala Trp Leu Leu Val Val Ala Phe Ala Val Val Gly Phe	
175 180 185	
tca ata gtc gtt tca aac ttt gga cct ttc atc acc tct ctt tac tgc	628
Ser Ile Val Val Ser Asn Phe Gly Pro Phe Ile Thr Ser Leu Tyr Cys	
190 195 200	
ctt ggt cta ttt ctt ggc act ata tat tct gtt cct cca ttc aga ctg	676
Leu Gly Leu Phe Leu Gly Thr Ile Tyr Ser Val Pro Pro Phe Arg Leu	
205 210 215	
aag aga tat cca gtt gct gct ttt ctt atc att gcg acg gtt cgt gga	724
Lys Arg Tyr Pro Val Ala Ala Phe Leu Ile Ile Ala Thr Val Arg Gly	
220 225 230 235	
ttc ctt ctc aac ttt ggg gtg tac tat gct act aga gct gca tta ggt	772
Phe Leu Leu Asn Phe Gly Val Tyr Tyr Ala Thr Arg Ala Ala Leu Gly	
240 245 250	
ctt aca ttc caa tgg agc tcg ccc gtt gct ttt att aca tgc ttt gtg	820
Leu Thr Phe Gln Trp Ser Ser Pro Val Ala Phe Ile Thr Cys Phe Val	
255 260 265	
aca gta ttt gct ctg gtc att gct ata acc aaa gat ctt ccg gat gtt	868
Thr Val Phe Ala Leu Val Ile Ala Ile Thr Lys Asp Leu Pro Asp Val	
270 275 280	
gaa ggg gac cgc aaa ttc caa ata tca act ttg gcg aca aag ctt ggt	916
Glu Gly Asp Arg Lys Phe Gln Ile Ser Thr Leu Ala Thr Lys Leu Gly	
285 290 295	
gtc aga aat att gcc ttc ctt ggc tct ggt tta ttg ttg gca aat tat	964

Val Arg Asn Ile Ala Phe Leu Gly Ser Gly Leu Leu Leu Ala Asn Tyr	
300 305 310 315	
ggt ggt gct att gta gta cct ttt ctt att cct cag gct ttc agg agc	1012
Val Val Ala Ile Val Val Pro Phe Leu Ile Pro Gln Ala Phe Arg Ser	
320 325 330	
ttt gta atg gtg cct ttt cat gct gct ctt gca gtt gct tta att ttt	1060
Phe Val Met Val Pro Phe His Ala Ala Leu Ala Val Ala Leu Ile Phe	
335 340 345	
cag aca tgg gtt ctg gag caa gca aag tac agt aag gat gct att tca	1108
Gln Thr Trp Val Leu Glu Gln Ala Lys Tyr Ser Lys Asp Ala Ile Ser	
350 355 360	
cag tac tac cgg ttc atc tgg aac ctc ttc tat gcc gaa tac atc ttc	1156
Gln Tyr Tyr Arg Phe Ile Trp Asn Leu Phe Tyr Ala Glu Tyr Ile Phe	
365 370 375	
ttc ccg tta ata tag agatatggcg ttgacatcg gctacacgat cggagcacgc	1211
Phe Pro Leu Ile *	
380	
accgaagcac gaattcggtt gggcaacaga agagaaaccc tttgtggtct ataaagcgtg	1271
agcaattttt gtacatactg ttgactggt aggggaatag agcggcgatg cgacgaggat	1331
cttgacgatg ctgtgggagg atccagtaga aaatgactga gttttcgtgg ttgtttctgc	1391
caacaaaaga ggaaaagaaa tgaaagtga aaggtatcgg gccttgttt ggagggattg	1451
gacgtaaaaa aaaaaaaaaa aaaaca	1477

<210> 28
 <211> 383
 <212> PRT
 <213> Triticum aestivum

<400> 28	
Met Ala Ser Leu Ala Ser Pro Pro Val Pro Ser His Ala Pro Thr Thr	
1 5 10 15	
Ala Ala Arg Phe Leu Pro Ala Pro Ala Gly Arg Gly Arg Arg Pro Ser	
20 25 30	
Pro Pro Ala Ala Ser Pro Ile Phe Ser Ser Ala Ser Thr Arg Phe Thr	
35 40 45	
Gln Ser Pro Arg Ala Pro Cys Gly Ala Ala Arg Pro Arg Trp Arg Asp	
50 55 60	
Thr Val Arg Ala Cys Ser Gln Ala Gly Ala Ala Gly Pro Ala Pro Leu	
65 70 75 80	
Ser Lys Thr Leu Ser Asp Leu Lys Asp Ser Cys Trp Arg Phe Leu Arg	
85 90 95	
Pro His Thr Ile Arg Gly Thr Ala Leu Gly Ser Thr Ala Leu Val Ala	
100 105 110	
Arg Ala Leu Leu Glu Asn Pro Gln Leu Ile Asp Trp Arg Leu Val Phe	
115 120 125	
Lys Ala Leu Tyr Gly Leu Val Ala Leu Ile Cys Gly Asn Gly Tyr Ile	
130 135 140	
Val Gly Ile Asn Gln Ile Tyr Asp Ile Gly Ile Asp Lys Val Asn Lys	
145 150 155 160	
Pro Tyr Leu Pro Ile Ala Ala Gly Asp Leu Ser Val Gln Ser Ala Trp	
165 170 175	
Leu Leu Val Val Ala Phe Ala Val Val Gly Phe Ser Ile Val Val Ser	

<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 31
agcgcggccg catggacgcg cttcgcctac ggccgt

36

<210> 32
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 32
agcgcggccg ctcaccgcac cagagggatg agcag

35